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EMBL; X73325; WBR.

HSSP; P01730; IWBR.

GO; GO:0042101; C:T-cell receptor activity; ISS.

GO; GO:004015026; F:GOTECEPTOR activity; ISS.

GO; GO:0015026; F:GOTECEPTOR activity; ISS.

GO; GO:00045086; P:MHC class II protein binding; ISS.

GO; GO:00045086; P:positive regulation of interleukin-2 biosyn. .; I

GO; GO:0010217; P:T-cell differentiation; ISS.

R GO; GO:0047059; P:T-cell selection; ISS.

R GO; GO:0007169; P:T-cell selection; T-cell; IMMINATE; SMO0406; IGv; I.

DR PRINTS; PRO0692; CD4TCANTIGEN.

SMART; SMO0406; IGv; I.

DR PROSTIE; PS50835; IG LIKE; I.

T Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

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T-CELL SURFACE GLYCOPROTEIN CD4.

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Hill R.L., Lebovitz H.E., Fellows (In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp Stockholm (1967).
-!- MISCELLANEOUS: Ref.1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit Igg: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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10-CCT-2003 (Rel. 42, Last annotation update)
Ig gamma chain C region.
Ig gamma chain C regionabbit).
Cryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Lagomorpha; Leporidae; Oryctolagus.
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PIR; A91749; GHRB.
HSSP; P01857; 1FC1
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Bernstein K.E., Alexander C.B., Mage
"Nucleotide sequence of a rabbit IgG
F-I haplotype.";
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"Sequence studies on the constant region immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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SIMILARITY: Contains 3 immunoglobulin-like domains.
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PS50835; IG_LIKE; 3.
PS00290; IG_MHC; 1.
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21-JUL-1986 (Rel. 01, Last sequence of the control of the control
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                                                                                SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
Turner K.J., Cebra J.J.;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
                                                         and hinge region cyanogen
Biochemistry 10:9-17(1971)
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PIR; A94553; G2GP.
HSSP; P01842; 7FAB.
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"Interchain disulfide bridg
Biochemistry 10:26-31(1971)
-!- MISCELLANEOUS: This cha
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Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 hom
antibodies.";
Biochemistry 13:4796-4803(1974).
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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MEDLINE=75036073; Pu
Trischmann T.M., Cel
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R EMBL; APO01226; AAB60873.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF057380; AAC5124.1; -.

R EMBL; AF057380; AAC5124.1; -.

R EMBL; AF057380; AAC5124.1; -.

R HSSP; P01730; IMIQ.

R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0042289; F:MC class II protein binding; ISS.

R GO; GO:0042289; F:MC class II protein binding; ISS.

R GO; GO:0045086; P:Do08itive response; ISS.

R GO; GO:0045086; P:Do08itive regulation of interleukin-2 bio

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.

R GO; GO:007169; P:transmembrane receptor protein tyrosine

R InterPro; IPR000973; CD4 TCA9.

R InterPro; IPR003596; Ig_v.

R Pfam; PF00047; Ig; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corbet 9., Barre-Sinoussi F., Allan J.S.;
Corbet 9., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
"Relation between phylogeny of African green monkey CD4
"Their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
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NCBI_TaxID=9534;
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                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Harris E.E., Disotell T.R.;
"Nuclear mane ****
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MEDLINE=98017879; PubMed=9379478;
Fommggaard A., Mueller-Trutwin M.C., Diop O., Hansen
Corbet S., Barre-Sinoussi F., Allan J.S.;
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"Molecular cloning and expression of african c
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
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Eur. J. Immunol. 22:2973-2981(1992).
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Catarrhini; Cercopithecidae;
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15-MAR-2004 (Rel. 4
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DIGIT
                          SEQUENCE OF 335-405 FROM N.A.
MEDLINE=8222190; PubMed=6283537;
MEDLINE=8222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T
Yamawaki-Kataoka Y., Nakai S.,
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                              Ig gamma-2B chain C
Mus musculus (Mouse)
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bulin domain; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                         TWTCTVLQNQKKVEFKIDIV
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19, Last sequence update)
43, Last annotation updat
C region, membrane-bound
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BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN
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S-palmitcyl cysteine (By similarity).

S-palmitcyl cysteine (By similarity).

S-palmitcyl cysteine (By similarity).

S-palmitcyl cysteine (By similarity).

N (IN REF. 3; AAB60875).

I -> T (IN REF. 3; AAB60873).

K -> E (IN REF. 3; AAB60873).

M -> V (IN REF. 3; AAB60873).

F -> L (IN REF. 3; AAB60873).

K -> B (IN REF. 3; AAB60873).

N -> H (IN REF. 3; AAB60873).

N -> H (IN REF. 3; AAB60873).
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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Sciurognathi; Muridae
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membrane
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; Murinae; Mus
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InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PSS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Transimon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rogers J., Cho
Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thie
                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identical with the corresponding region of the secreted form. MISCELLANEOUS: The a allele sequence is shown. SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Membrane-bound;
IsoId=P01867-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1CIC; 11-MAR-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C02154; G2MSBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration -
                       133
                                             229
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M: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS SCELLANEOUS: The sequence of residues 1-335 is assumed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P01866-1; Sequence=External;
                                                                                                                                                                          Similarity
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                     PRIKOVLMISLTPKVTCVVVDVSEDDDDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
                                  PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                   QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
                                                                                         ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                                                                                LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
                                                                                                                                      LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
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51.7%;
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Pred. No. 4.
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CYTOPLASMIC
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IG-LIKE 2.
IG-LIKE 3.
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                                                                                                                                                                                                         89B3CF0A9B6D49FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-AUG-1991
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SMART; SM00407; IGc1;
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InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                           162;
                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                 Similarity
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                       LGGPSVFLFPPXPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                           SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----
                                                                                                                                                                                                                        SVSQLELQDSGTW----TCTVLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCP--EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDV
                                                                           LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCNVRHEGLKNYYLKKTISRSPGLDLDDICAEAKDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                        224
329 AA;
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                                                                                                                                                                                                                                                                                                                                                                      113 H3
223 CH
327 CK
36228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig-like.
Ig_c1.
Ig_MHC.
                                                                                                                                                                                                                                                                                               31.7%;
                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                          CH1.
CH2.
CH3.
                                                                                                                                                                                                                                                                                               Score 857.5; DB 1
Pred. No. 6.8e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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Matches 157
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101-FEB-1991 (Rel. 17, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
1111 gamma-28 chain C region.
1111 Rattus norvegicus (Rat).
1111 Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Murinotai TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J_RAT
                                                                                                                                                                                                                                                                                                                                                    PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                            GCB RAT
P20761;
01-FEB-1991
01-FEB-1991
10-OCT-2003
                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immuno
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 Gene 74:473-482(1988).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Brueggemann M.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Evolution of the rat immunoglobulin gamma heavy-chain gene
                                                                                                                                                           Local Similarity
 245
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                                                                                                                      SGTW-----TCTVLQ--NQKKVEFKIDI------VPCPAPEPKSCDKTHTC--PELLGGP
         TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                  SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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TEQTVSLTCLTSGFLENDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLNVERSRWD
                                                                       SVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQPREEQYNS
                                                                                                            SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSWLQGEIFTCSVVHEALHNHHTQKNLSRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
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INTERCHAIN
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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                                                                                                                                                                                     55F8B64D48D460A6 CRC64;
                                                                                                                                                 Mismatches
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No. 2.
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HLIM)
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Best Local S
Matches 163
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DISULFID
SEQUENCE
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DOMAIN
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InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 74:473-482(1988)
PIR; PS0017; PS0017.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GC1_RAT STANDARD; PRT; 2
P20759; (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig gamma-1 chain C region.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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[1]
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brueggemann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89232738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolution of the
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240
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                                                                                                                                                                                                163;
                                                                                                                                                          28
                                                                                                                                                                                                          Similarity
         NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                              LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LQSGLYTLTSSVTV-PSSTWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGNVFSCSVMHEALHNHYTQKSLSLSPG
                                               RVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                                                                                                                    QTVTCNVAHPASSTKVDKKI-----VPRNC------GGDCKPCICTGSEVSSV
                                                                                                                                                                            LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                       FLFPPKDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
NEVSITCMVKGFYPPDIYVEWQMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKEKWQQG
                                     RSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMS
                                                                            FIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTF
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                domain;
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CH2.
CH3.
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Pred. No. 1e-45;
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013BAB45EF49B9DA CRC64;
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SMART; SM00407; IG¢1; 2.
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PIR; S00847; S00847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., C.
"Sequence of a rat immunoglobulin gamma 2c heavy chi
region cDNA: extensive homology to mouse gamma 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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QHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYTIPPPREQMSKNKVSLTCM
                                  LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
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                                                                                                                                                                                                                                                                                                "Evolution of immunoglobulin subclasses. murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (MYELOMA PROTEIN MOPC MEDLINE=78242288; Pubmed=98524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mano Y., Seidman J.G., Peterlin B.M.
"Immunoglobulin gamma 1 heavy chain
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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Honjo T., Obata M., Yamawaki-Kataoka
Takahashi N., Mano Y.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel.
15-MAR-2004 (Rel.
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-i- SUBCELLULAR LOCATION: Secreted.
-i- ALTERNATIVE PRODUCTS:
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Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
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EMBL; V00795; CAA24176.1; -.
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- MOUSE
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PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immuno
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PIR; A02152; G2MSA.
PDB; 124W; 12-JUL-01.
PDB; 184X; 12-JUL-01.
PDB; 1MNU; 06-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-74175517; PubMed=4831970;
Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Implications
for the evolution of immunoglobulin structure and function.";
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MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete nucleotide sequence of mouse immunoglobin gamma 2a gen and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
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"Structure of the constant and 3' untranslated
Balb/c gamma Za heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                     Immunoglobulin
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"Determination of the primary structure of a mouse gamm immunoglobulin. Identification of the disulfide bridges Eur. J. Biochem. 30:452-462(1972).
-i- SIMILARITY: Contains 3 immunoglobulin-like domains.
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family.";
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MEDLINE=81076554; PubMed=6777755;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Best Local &
Matches 155
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Schreiter P.H., Bothwell A.L.M., Mueller-Hill B.,
"Multiple differences between the nucleic acid se
IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                MEDLINE=82037777; PubMed=6794027;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine chain Fc regions of Igla and Iglb allotypic forms.
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                     IsoId=P01865-1; Sequence=External; MISCELLANEOUS: The sequence differs from that of the from BALB/c mice, at 15% of the positions. SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                           Note=Probably the major isoform;
Name=Membrane-bound;
                                                                                                                                        Name=Secreted;
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              SWISS-PROT entry is
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B84361C5445A6864 CRC64;
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Sciurognathi; Muridae;
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01-FEB-1991
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DOMAIN
SEQUENCE
                   SEQUENCE FROM N.A. MEDLINE=89232738;
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
10-OCT-2003 (Rel. 42, Last ann
1g gamma-2A chain C region.
Rattus norvegicus (Rat).
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG LIKE; 3
PROSITE; PS00290; IG MHC; 1.
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; 1HH6; 26-JAN-01.
; 1HH9; 24-JUL-03.
; 1HI6; 08-FEB-01.
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335 AA;
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Rodentia;
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annotation
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Pred. No. 2.
                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 19; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M13804; AAA41376.1; ALT_INIT. PIR; PS0019; PS0019. HSSP; P01842; 7FAB.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                 LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LOSGLYTLTSSVTV-PSSTWSS
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                                                                                                                                                               HNHYTQKSLSLSPG 431
                                                                                                                                                                                                           YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
                                                                                                                                                                                                                                                                                     ITLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVHRD
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(Rel. 34, Last sequence update)
(Rel. 42, Last annotation updat
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                              glycoprotein
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51.0%;
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                              CD4
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Pred. No. 9.4e
17; Mismatches
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INTERCHAIN
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IG-LIKE
                              tation update)
 (T-cell surface antigen T4/Leu-3)
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HTIW)
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R EMBL; X73328; CAA51754.1; -.

R EMBL; X73327; CAA51753.1; -.

R HSSP; PO1730; IMIQ.

R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0042101; C:T-cell receptor activity; ISS.

R GO; GO:0042289; F:MHC class II protein binding; ISS.

R GO; GO:0006955; F:MHC class II protein binding; ISS.

R GO; GO:0006955; F:Immune response; ISS.

R GO; GO:00045086; P:Positive regulation of interleukin-2 biosyn...

R GO; GO:0045086; P:T-cell differentiation; ISS.

R GO; GO:0045088; P:T-cell selection; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunodeficiency virus.";
Bur. J. Immunol. 22:2973-2981(1992).
-i- FUNCTION: Accessory protein for WHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSSO835; IG LIKE; 1.
Immunoglobulin domain; Transmembrane;
Immune response; Repeat; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00692; CD4TC/
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the By non-profit institutions as long as its content is in no way as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93049640; PubMed=1425921;
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SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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BY SIMILARITY.
BY SIMILARITY.
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S-palmitoyl cys
S-palmitoyl cys
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V -> M.
V -> M.
R -> K.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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(See http://www.isb-sib.ch/announce/
                                                                                                                                      cysteine cysteine
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(POTENTIAL).
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similarity)
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                           GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0042101; C:T-cell receptor activity; ISS.
GO; GO:0042289; F:MFC class II protein binding; ISS.
GO; GO:0042289; F:MFC class II protein binding; ISS.
GO; GO:0045086; P:Desitive regulation of interleukin-2 bio
GO; GO:0030217; P:T-cell differentiation, ISS.
GO; GO:0045086; P:T-cell selection; ISS.
GO; GO:0045089; P:T-cell selection; ISS.
GO; GO:0007169; P:transmembrane receptor protein tyrosine
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR0001010; Ig-Tike.
R InterPro; IPR000110; Ig-Tike.
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                                                                                                                       EMBL; X73324; C
HSSP; P01730; 1
GO; GO:00042101;
GO; GO:0015026;
GO; GO:0042289;
GO; GO:0045086;
GO; GO:0045086;
GO; GO:0030217;
GO; GO:0005030217;
GO; GO:0005086;
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GO; GO:0005086;
GO; GO:0005086;
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Q08339;
01-FEB-1995
01-FEB-1995
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fomsgaard A., Hirsch V.M., Johnson P.I. "Cloning and sequences of primate CD4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restroy by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p55-lck (By similarity).
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Tucker P.W., Marcu K.B., Newell N., F
"Sequence of the cloned gene for the
2b immunoglobulin heavy chain.";
Science 206:1303-1306(1979).
                                                            MEDLINE=80081502; PubMed=117549;
MEDLINE=80081502; PubMed=117549;

MARCU K.B., Newell N.,
                                                                                                                                                    Tucker P.W., Marcu K.B., Slightom J.L., Blattne "Structure of the constant and 3' untranslated gamma 2b heavy chain messenger RNA."; Science 206:1299-1303(1979).
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MEDLINE=80081501; PubMed=117548;
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MEDLINE=80120716; PubMed=6766534;
Yamawaki-Kataoka Y., Kataoka T.,
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Mammalia; Eutheria; Rodentia;
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Ig gamma-2B chain
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Immune response; Repeat; Lipoprotein; Palmitate.
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SMART; SM00407; IGc1; 2.
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Kim H., Yamaguchi Y., Masuda K., Matsunaga
Irimura T., Takahashi N., Kato K., Arata Y
"O-glycosylation in hinge region of mouse
J. Biol. Chem. 269:12345-12350(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Note=May be the major isoform;
Name=Membrane-bound;
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se immunoglobulin allotypes:
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 229
                                         183
                                                                                                     161;
                    78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma 2b chain ge
296:761-763(1982)
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                 PS50835; IG_LIKE; 3.
PS00290; IG_MHC; 1.
ps00290; IG_MHC; 1.
psudin domain; Immunoglobulin C region; Glycoprotein;
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                    QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
                                       ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                            LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
                                                                        LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW---
                                                                                                                                          239
336
                                                                                                                                                                                                                                                                                 127
235
15
27
109
112
115
                                                                                                                                                                                                                   118
150
256
105
163
                                                                                                                                                                                                                                                                                                                                                                          aplicing; Repeat.
                                                                                                     Conservative
                                                                                                                                              $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=6803173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALLELE
                                                                                                                                             239
36658
                                                                                                               28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                     50,
                                                                                                                                                    REMOVED
Q -> R
Q -> R
I -> R
I -> R
I -> R
I -> R
                                                                                                               Score 781.5;
Pred. No. 5e-
                                                                                                                                                                                                                                                                     INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                                                                                                                                                                        IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
                                                                                                                                                                                                                                                                                                                                 IG-LIKE
IG-LIKE
                                                                                                                                                                                                                                        O-LINKED
                                                                                                                                           REMOVED POST-TRANSLATIONALLY ()
Q -> R (IN ALLELE B).
T -> A (IN ALLELE B).
N -> D (IN ALLELE B).
M -> I (IN ALLELE B).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
7D879662607C356E CRC64;
                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsunaga
Arata Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         post-duplication divergence of gamma
                                                                                                                             IN ALLELE B).

1 ALLELE B).

1 ALLELE B).

1 ALLELE B).

REF. 2 AND 3).

REF. 2 AND 3).

TC356E CRC64;
                                                                                                                                                                                                                                        (GALNAC
                                                                                                              5e-43;
                                                                                                                                                                                                                                                                      HLIM)
HLIM)
HLIM)
                                                                                                                                                                                                                                                                                                                          HTIW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin G2b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C., Yamamoto
                                                                                                                       DB 1;
                                                                                                     73;
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                                                                                                                                                                                                                                                                                                                        A LIGHT
                                                                                                                                                                                                                                                                     HEAVY
HEAVY
HEAVY
HEAVY
                                                                                                     Indels
                                                                                                                       Length
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CHAIN)
CHAIN)
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                                                                                                                         336;
                                                                                                                                                                                                                              (PROBABLE)
                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SI
                   132
                                         228
                                                             77
                                                                                182
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RESULT
CD4_SAI
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   CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                     GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015226; F:coreceptor activity; ISS.
GO; GO:0015226; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:000655; P:immune response; ISS.
GO; GO:0005085; P:prositive regulation of interleukin-2
GO; GO:00030217; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0007169; P:transmembrane receptor protein tyrosin
                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4 SAISC
Q29037;
                                                           Immune
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, 25, 01-NOV-1997 (Rel. 42, Last a. 10-OCT-2003 (Rel. 42, Last a. 10-OCT-2003)
                                                                                                                                                                                                                                                                                                                        EMBL; D86588; BAA13131.1; -. HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                          InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatsumi M., Hashimoto
Submitted (AUG-1996)
                                                                                                       PROSITE;
                                                                                                                      SMART;
                                                                                                                                PRINTS;
                                                                                                                                              Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9521;
                                                                                        mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Accessory protein for MHC class-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313
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                                                                                                                ; PR00692; CD47
SM00406; IGV;
                                                                                                     PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDV
                                                                                                                                                1g;
                                                                                      domain; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                          Repeat;
                                                                                                                                  CD4TCANTIGEN
   25
457
395
417
457
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Last annotation updat
protein CD4 precursor (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
Signal; Lipoprotein; Palmitate.
BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
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rsor (T-cell surface antigen
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                                                                                                                                                                                                        protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen/T-cell
                                                                                      T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
Cebinae; Saimiri.
                                                                                                                                                                                                                                                 biosyn.
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                                             CD4
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Best Local S
Matches 209
                                                                                                      CD4 CANFA
P33705;
01-FEB-1994 (Re:
01-FEB-1994 (Re:
15-MAR-2004 (Re:
T-cell surface:
                                                                                                                                                                        CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
DISULFID
DISULFID
DISULFID
SEQUENCE
SEQUENCE OF 13-463 FROM N.A. STRAIN=Beagle; TISSUE=Thymus; MEDLINE=93192324; PubMed=7916
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                       NCBI_TaxID=9615;
                                                                           Canis familiaris
                                                                                               T4/Leu-3).
                                                                                                                                                                                                                 387
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                                                                                                                                                                                                                                                                                                                                                                NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                                                                                                                                                       င္
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVFGLTANPDTHLLQGQSLTLTLESPPGSSPSVECTSPRGKRIRGRKTLSVSQLGIPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                     HYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDP-PRASALPAPPTGSALPDPQTASAL
                                                                                                                                                                                                                                                                                                                                            --QDPKLRMGKK---LPLHLTLAQALPQYAGSGNFTL-----ALKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNGGIFFRHLLLVLQLALLPAVTHGKTVVLGKKGEVVELFCETSLKKKNVFFHWKTSDQIK
                                                                                                                                                                                                                 PTRSPPVQ---PMVLIVLGGVAGLLAFTGLGIFLCVRCRHR
                                                                                                                                                                                                                                     P--DPPAASALPAALAVISFLLGL----GLGV-ACVLARTR
                                                                                                                                                                                                                                                           --TSPKLMLS
                                                                                                                                                                                                                                                                                                                       SDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                                                                                                                                          RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                                                                                                                                                                                                                                                                                                                                                                                                              TWKCTVFQHLELV-FEINIVVLAFQQASS----TVYKKEGEQVEFSFPLAFAAETLIGS
                                                                                                      4 (Rel. 28, Create
4 (Rel. 28, Last s
4 (Rel. 43, Last a
face glycoprotein (
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203
217
254
254
418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā,
                                                                                                                                                             STANDARD;
                                                    s (Dog).
zoa; Chordata; C
ria; Carnivora;
                                                                                                28, Createa,
28, Last sequence update)
43, Last annotation updat
vcoprotein CD4 precursor (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
202
316
373
373
373
254
1109
1184
4184
4218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%;
                                                                                                                                                                                                                                                          -LKLENQEAKVSKRE-KAVWVLNPEPGAWQCLLSDSGQVLLESK-FEAL
                                                                                                                                                                                                                                                                                                                                                                                     ----ELCW-----QAERASSSKSWITFNLTKQEVYVKLVT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
N-LIKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S-Palmitcoyl cysteine (
S-Palmitcoyl cysteine (
S-Palmitcoyl cysteine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 743; DB 1;
Pred. No. 2.1e-40;
6; Mismatches 150
                                                 Craniata; Vez; Fissipedia;
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                   ----GKLHQEVNLVVMRVTQLQNNL-TCEVWGP----
                                                                                                      tation update)
precursor (T-cell
                                                                                                                                                             463
                                                    Vertebrata;
ia; Canidae;
                                                                                                                                                             ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By
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                                                                                                         surface
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                                                               Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
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                                                                                                        antigen
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Query Match
Best Local S
Matches 177
                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 3.
PRINTS; PR00692; CD4TAN
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIK
Immunoglobulin domain; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Beagle; TISSUE=Thymus;
MEDLINE=94378217; PubMed=8091416;
Gorman S.D., Frewin M.R., Cobbold S.P., Waldmann H.;
"Isolation and expression of cDNA encoding the canine CD4 alpha antigens.";
Tissue antigens.";
                                                              CARBOHYD
CARBOHYD
                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                     DOMAIN
DISULFID
DISULFID
LIPID
                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01730; 1WBR. —

GO; GO:0042101; C:T-Cell receptor complex; ISS.

GO; GO:0015026; F:coreceptor activity; ISS.

GO; GO:0015026; F:coreceptor activity; ISS.

GO; GO:0042289; F:MHC class II protein binding; ISS.

GO; GO:0006955; P:immune response; ISS.

GO; GO:0006955; P:jositive regulation of interleukin-2

GO; GO:0030217; F:T-cell differentiation; ISS.

GO; GO:0045058; P:T-cell selection; ISS.

GO; GO:0045059; P:T-cell selection; ISS.
                                                                                                                             LIPID
CARBOHYD
                                                                                                                                                                                                                                                                                    Immune
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. The transfer of restrictions the European Experimental State of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: Expressed in macrophages and a subset o
                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000973; CD4_TCAg.
InterPro; IPR007110; Ig-Tike.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T lymphocytes.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domain
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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P01730; 1WBR.
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                                                                                                                                                                                                                                                                                                response; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F., Conner G.E., Minz D.H., Alejandro R structure of the canine CD4 antigen."; Biophys. Acta 1172:315-318(1993).
                                                  CD4TCANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOT_ANNOTATED_CDS.
            22.9%;
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t; Signal; Lipoprotein; Palmitate.
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                                                          BY SIMILARITY.

S-palmitcyl cysteine (By S-palmitcyl cysteine (B) N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)

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N-LINKED (GLCNAC...)
                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTI
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 3
BY SIMILARITY.
BY SIMILARITY.
 Score 617.5; DB Pred. No. 2.2e-3 B; Mismatches 1
                                                                                                                                                                                                                                                                       T-CELL SURFACE GLYCOPROTE EXTRACELLULAR (POTENTIAL)
                                                    95805170CB44A833
                                                                                                                                                                                                                                                                                                                                                                                                                             receptor protein tyrosine
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                                                             D (GLCNAC...) (POTENTIAL).
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(By similarity)
(POTENTIAL).
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Similarity

Conservative

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Gaps

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P46630;
Ol-NOV-1995 (Rel. 32, Created)
Ol-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface
                                                                                                                                                                                                     immunodeficiency virus type 1.";

Proc. Natl. Acad. Sci. U.S.A. 89:7963-7967(1992).

Proc. Natl. Class-II antigen/T-cell activation.

Proc. Natl. Acad. Sci. U.S.A. 89:7963-7967(1992).

Proc. Natl. Acad. Sci. U.S.A. 89:7967(1992).

Proc. Natl. Acad. Sci. U.S. 89:7967(1992).

Proc. Natl. Aca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92390370; PubMed=1518821; Hague B.F., Sawabdikosol S., Brow Kindt T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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GO; GO:0042286; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:004289; P:immune response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO; GO:0045086; P:T-cell differentiation; ISS.
GO; GO:0030217; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0692; CD4TC; SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M92840; AAA31198.1; -. PIR; A46254; A46254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01730; 1WBR.
                     352
                                                                                       230
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304
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                                                                                                            236
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                                                                                                                                                                                                                                                                                        1 MNRGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response;
                                                                                                                                                                                                                                                                                                                                  Similarity
                                           SAQSWVSFSLEDRKVSVQKILP---DLKIQMSKGLPLS---LTLPQALHRYAGSGNLSLT
                     CLVKG
                                                                                                                                                                                            EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                                                                                                 ILGNQG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
-LDKG
                                                                 LHQDWLNGKEYKCKVS-NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT-KNQVSLT
                                                                                                            LMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                   QDSGTWSCHLSFQDQNKLELDIKIIVLGFPKASA----
                                                                                                                                                        QDSGTWTCTV-LQNQKKVBFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                               EVELLVFRLTANPNTRLLHGOSLTLTLEGPSVGSPSVQWKSPENKIIETGPTCSMPKLRL
                                                                                                                                                                                                                            ILGNQGSSSSFWLKGNSPLSNRVESKKNMWDQGSFPLVIKDLRMDDSGTYICEVGDKKM
                                                                                                                                                                                                                                                                        MNRRIYFQCLLLVLPLALLPAATWGKTVVRGKAGAIVELPCQSSQKRNSVFNWKHANQVK
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                                                                                       -LNFEDESLSGELMWQVDGAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
S-palmitoyl cysteine (By sepalmitoyl cysteine (By S-palmitoyl cysteine (By B323311CBD40013D CRC64;
                                                                                                                                                                                                                                                                                                                     Pred. No. 2.3
1; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 601.5;
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC.
                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                            similarity).
similarity).
                                                                                                                                                                                                                                                                                                                                           459;
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RESULT 32 CD4\_RAT ID CD4\_RAT

STANDARD;

457

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R EMBL; M15768; AAA40901.1; -.

R PIR; A27449; A27449.

R PDB; 1CID; 15-JUL-93.

R GD; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0042101; C:T-cell receptor activity; ISS.

R GO; GO:0042289; F:MHC class II protein binding; ISS.

R GO; GO:0040289; F:MHC class II protein binding; ISS.

R GO; GO:0045086; P:positive response; ISS.

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.

R GO; GO:007169; P:transmembrane receptor protein tyrosine

R InterPro; IPR000710; Ig-Iike.

R InterPro; IPR003599; Ig.

R Pfam; PF00047; ig; 2:

R Pfam; PF00047; ig; 2:
DOMAIN
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CARBOHYD
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Peptide and nucleotide sequences of rat CD4 (W3/25) evidence for derivation from a structure with four immunoglobulin-related domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05540;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell T4/Leu-3) (W3/25 antigen)
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MEDLINE=87175535; PubMed=3104900;
Clark S.J., Jefferies W.A., Barclay A.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NH2-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
WEDLINE=93267437; Pubmed=8493535;
Brady R.L. Dodson E.J. Dodson G.G.
Williams A.F. Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin-related domains.";
Proc. Natl. Acad. Sci. U.S.A. 84:1649-1653(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                ; PR00692; CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                   PS50835; IG_LIKE; 1.
obulin domain; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure of domains 3 and 4
                                                                                                                                                      Repeat;
                                                                                                                                                                                                                CD4 TCANTIGEN
                                                                                                                                                   Transmembrane; Glycoprotein; T-cell; signal; Lipoprotein; Palmitate; 3D
           EXTRACELLULAR (POTENTIAL POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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Sciurognathi; Muridae;
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(GLCNAC.
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(POTENTIAL)
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; Murinae; Rat
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MBL outstation -
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RESULT 33
CD4_MOUSE
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                                                                                                                                                                                                                                                                                        MNRGVPFRHL--LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                                                     ----POVSLOFAGSG----NLTLT---LDR-GILYQEVNLVVMKVTQPDSNTLTCEVM
                                                                                                                                                                                                                          QLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ
                                                                                                     GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                    QSWITFSLKNOKVS
                                                                                                                                  QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
                                                                                                                                                                  LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                  DSGIWN
                                                                                                                                                                                                DSGTWTCTVLQNQKKVEF--KIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                ELWVFRVTFNPGTRLLQGQSLTLILDSNPKVSDPPIECKHKSSNIVKDSKAFSTHSLRIQ
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                                                                                                                                                                                                                                                                              MCRGFSFRHLLPLLLLQLSKLLVVTQGKTVVLGKEGGSAELPCESTSRRSASFAWKSSDQ
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N-LINKED (GLCNAC...)
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
S-palmitoyl cysteine (
S-palmitoyl cysteine (
                                                                                                                    ---VOKSTSNPKFOLSE-
                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                             Score
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.5e-24;
                                                                                                                                                                                                                                                                                                                           Length
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(By similarity)
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                                                                                                                                                                                                                                                                                                                             457;
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                                                                                                                                                   249
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CD4\_MOUSE STANDARD; PRT; 457 AA. PD6332; 01-JAN-1988 (Rel. 06, Created) 01-JAN-1988 (Rel. 06, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) T-cell surface glycoprotein CD4 precursor (T-T4/Leu-3) (T-cell differentiation antigen L3T-T4/Leu-3)

antigen L3T4)

(T-cell

surface

antigen

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Uddin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Toung A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shevchenko Y., Smailus D.E.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
RT Thuman and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJUE-98112780; PubMed=9445485;
Ansari-Lari M.A., Oeltjen J.C., Schwartz
Lu J., Gorrell J.H., Chinault A.C., Belmc
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative sequence analysis of chromosome 12pl3 and its syntenic Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Unusual intron in the immunoglobulin domain of the newly isolated murine CD4 (L3T4) gene."; Nature 325.453-455(1987).
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MEDLINE=87115821; PubMed=3027575;
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MEDLINE=87018845; PubMed=3094146;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                   SEQUENCE
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                               MEDLINE=86166694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Littman D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain.";
=86166694; PubMed=3082751;
B.J., Tsagaratos J., Kirs
M., McKenzie I.F.C., Walk
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Kirszbaum L
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nervous system.";
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Belmont J.W., Miller W.,
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J CD4 and
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                 Maddox
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EMBL; M36850; AAA39401.1; -.
EMBL; M13816; AAA37267.1; -.
EMBL; X04836; CAA28539.1; -.
EMBL; M36851; AAA39402.1; -.
EMBL; M17080; AAA37403.1; -.
EMBL; M17070; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; -.
EMBL; M2002397; AAC36010.1; -.
EMBL; BC039137; AAH39137.1; -.
EMBL; BC039137; AAH39137.1; -.
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GO; GO:0015226; F:coreceptor activity; ISS.
GO; GO:0015226; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0042289; F:immune response; ISS.
GO; GO:004508; P:positive regulation of interleukin-2 biosyn.
GO; GO:0030217; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0045058; P:transmembrane receptor protein tyrosine kin.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR000973; GD4 TCAg.
InterPro; IPR003596; Ig_v.
DEAUTICE. DEDOGES: COATCONTICEN
                                                                                                                                                                               SMART; SMO406; IGv; 1.
SMART; SMO406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
Immunoglobulin domain; Signal; Lipoprotein; Palmitate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor interaction, May regulate T-c
-!- SUBUNIT: Associates with p56-lck (By s
-!- SUBCELLULAR LOCATION: Type I membrane
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Classon B.J., Tsagaratos J., McKenzie I.F.C., Wal "Partial primary structure of the T4 antigens of assignment of intrachain disulfide bonds ", Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Accessory protein for MHC class-II antigen/receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2; Synonyms=Brain-specific;
ISOId=P06332-2; Sequence=VSP 002489;
SIMILARITY: Contains 3 immunoglobulin-like
SIMILARITY: Contains 1 immunoglobulin-like
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IG-LIKE C2-TYPE 2.
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V-type domain.
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RESULT 34

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TO 196336; P01856;

DT 21-JUL-1986 (Rel. 01, Created Profiles (Rel. 33, Last as 1 196336;

DT 15-JUL-1999 (Rel. 38, Last as 1 196336;

DT 15-JUL-1999 (Rel. 38, Last as 1 196336;

DT 15-JUL-1999 (Rel. 38, Last as 1 19636;

DT 15-JUL-1999 (Rel. 38, Last as 1 19636;

Eukaryota; Metazoa; Chordata;

OC Mammalia; Eutheria; Rodentia,

OC Mammalia; PubMed=632;

RA MEDLINE=83117774; PubMed=681;

RA Honjo T.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=84236092; PubMed=6329728; Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.; Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.; "The nucleotide sequence of the mouse immunoglobulin epsilon comparison with the human epsilon gene sequence."; EMBO J. 1:1117-1123(1982).
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MEDLINE=83117774; PubMed=6818553;
Liu F.-T., Albrandt K., Succliffe
"Cloning and nucleotide sequence c
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an email to license@isb-sib.ch).
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PROSITE; PS00290; IG_MHC; 3.
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Homo sapiens

(Human)

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This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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SEQUENCE OF 1-434 FROM N.A.
MEDLING=90332450; PubMed=2115996;
Friedlander R.M., Nussenzweig M.C., L
                                                                                           GlycoSuiteDB; P01871; -..
GO; GO:0005624; C:membra
GO; GO:0003823; F:antige
GO; GO:0006955; P:immune
                                                                                                                                                                               EMBL; X17115; CAA34971.1; ALT SEQ. EMBL; X57086; -; NOT_ANNOTATED_CDS HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                   chain cDNA from B cells and mouse-human hybridomas.";
Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
-i- MISCELLANEOUS: All 4 combinations of the S/G and V/G
at positions 192 and 216 have been observed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).

MEDLINE=75059123; PubMed=4803843;

Watenable S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;

"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain
(pape), subgroup H III. Architecture of the complete IgM-molecule.

Lype), subgroup H III. Architecture of the complete IgM-molecule.

Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbitte T.H., Forster A., Mistein C.P.; "Human immunoglobulin heavy chain genes: evolutionary C mu, C delta and C gamma genes and associated switch Nucleic Acids Res. 9:4509-4524(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (WALDENSTROM'S OU),
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Dolby T.W., Devuono J., Croce C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 299-387 AND 438-454 FROM
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MEDLINE=82059479; PubMed=6795593;
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Mammalia; Eutheria;
                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                      olby T.W., Devuono J., Croce C.M.; Cloning and partial nucleotide sequence of human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete amino acid sequence
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rPro; lrnvv., 1g; 4.
A; PRO0047; 1g; 4.
RT; SM00407; IGC1; 3.
                                                                                         GO:0005624; C:membrane fraction
GO:0003823; F:antigen binding;
GO:0006955; P:immune response;
                                                                                                                                               147020; - 1701.
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                                  ILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                                                                    SRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYS
                                                                                                       HPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPP
                                                                                                                      QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPP
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                                                  KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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A02167; M
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European Bioinformatics Institute.
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MISCELLANEOUS: The sequence of resid
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Secreted;
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MEDLINE-82174576; PubMed-6803238;
Hellman L., Pettersson U., Bennich H.;
"Characterization and molecular cloning of the mRNA for (epsilon) chain of rat immunoglobulin E.";
Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
-!- SIMILARITY: Contains 4 immunoglobulin-like domains.
              This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                             MEDLINE=83182019;
                                                                                                                                                                                                                                                                                                                                                                    Hellman L.,
                                                                                                                                                       SEQUENCE OF 205-306 FROM
                                                                                                                                                                                                          "A cloned cDNA probe for rat construction, identification,
                                                                                                                                                                                                                                           Kindsvogel W.R.,
                                                                                                                                                                                                                                                                                SEQUENCE OF 168-342 FROM
                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 10:6041-6049(1982).
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83064537; PubMed=6292865;
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                 Hellman L., Pettersson U., Engstroem A., "Structure and evolution of the heavy ch
the
Swiss
                                                                                                                                                                                                          Reddy E.P., Moore J.M., Faurobe for rat immunoglobulin entification, and DNA sequer
                                                                                                                                                                                                                                                             PubMed=6820340;
Institute
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003065; Ig_MHC.
Pfam; PF00047; ig; 4.
SMART; SM00407; IGcl; 1.
PR0SITE; PS50035; IG_LIKE; 4.
PR0SITE; PS00290; IG_MHC; 3.
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P04221;
                    SEQUENCE FROM N.A. (A2 ALLOTYPE).

MEDLINE=84088930; PubMed=6418803;
MEDRINE=14088930; PubMed=6418803;
MEDRINE=14088930; PubMed=6418803;

"Complete sequence of a cloned cDNA encoding rabbit sec of VHa2 allorype: comparisons with VHa1 and membrane muj. Immunol. 132:490-495(1984).

-i- ALTERNATIVE PRODUCTS:
                                                                                                                               20-MAR-1987 (Rel. 04, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 mu chain C region membrane-bound form.
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entitles requires a license acrossor
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PIR; A93442; EHRT
HSSP; P01854; 1IG
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                                                                                                                     NCBI_TaxID=9986;
Event=Alternative splicing; Named isoforms=2; Comment=During differentiation, B lymphocyt
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EEEE--KDKRTLTCLIQNFFPEDISVQWLQDSKLIPKSQHSTTTP-LKYNGSNQRFFIFS
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lymphocytes
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MIC; 3.
Immunoglobulin domain; Immunoglobulin C region;
Alternative splicing; Transmembrane.
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PIR; A02165; MHRBM.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                Similarity
VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK
                                FFDKNVSMSSECSTTPSP
                                                                                                                                 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR------
                                                                                                                                                                          NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL
                                                                                                                                                                                                                  AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
                                                  ONOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                       SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
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IPR003006; Ig_MHC.
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C
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P01874;
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HSSP; P01857; 1FC1
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"Amino acid sequence of the Fc region of a canine interspecies homology for the IgM class.";
Science 200:1159-1161(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 178-450 (MOO). 
MEDLINE=78180587; PubMed=653360;
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"The complete amino-acid sequence
Mol. Immunol. 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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Canis familiaris (Dog).
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
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TNEVZAZAKZSGPTTYKVTSMLTIQEDAWLSQSVFTCKVEHRGLTFQQNASSM---
                                           LSVSQLELQDSG-----
                                                                                                                                        QGQSLTLTLESPPGSSPSVQCR-----
                                                                                                                                                                               SVLRGGKYVATSQVFLPSVDIIQGTDEHIVCKVRHSBGBKQKBVPLPVM------
                                                                                                                                                                                                                                                                                 TVAMGCLARDFLPGSITFSWKYEBLSAINSTRG-----
                                                                                                                                                                                                                                                                                                                               TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPHMVTERTVDKS----TEGEVGAEEEGFENLWTT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 AA; 48895 MW;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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. 01, Last
. 38, Last
                                                                                          PPEVSGFIPPRDAFFGBPRKSQLICQASGFSPRQVWSLRDGKQIESGVT
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24.1%;
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annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Score 369; DB 1;
Pred. No. 1.6e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                      -GKNIQGGKT 168
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Best Local
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P04220;
20-MAR-1987
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HUMAN
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SEQUENCE
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DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Ver Mammalia; Eutheria; Primates; Catarrhini; H
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin 100MAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02163; MHHUBT. HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of mu-chain-disease protein BOT. amino-acid sequence of the N-terminal 42 positions."; Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0006955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005624;
GO; GO:0003823;
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KLICQATGFSPRQIEVSWLREGKQVGSGVTTDEVEAEAKESGPTTYKVTSTLTIKESDWL 128
                                         -----SPR-----
                                                                                        EAEDRIIKEEEARL----
                                                                                                                             EVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR------
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                                                                                                                                                                                                                                                                 262
391
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                           domain; Immunoglobulin
42 PRE-C-PAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P:immune response;
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F:antigen k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=6425189;
S., Mihaesco E.,
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261
391
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                                                                                                                                                                                                  13.5%;
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                                                                                                                                                                                                                                                               noglobulin C region.
PRE-C-PART (NO V REC
CH2.
CH3.
CH4.
CH4.
W; 9100843AF0CF021A C
                                                                                                                                                                         Score 365.5; DB 1;
Pred. No. 2.3e-16;
5; Mismatches 132;
                                                                                     -SGRD----MQVTSQPVIAELPPKVSVFVPPRDGFFGNPRKS
                                     -GKNIQGGKTLSVSQLELQDSG-----
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RESULT 41
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MEDIJINE=81076590; PubMed=6255422;
MEDIJINE=81076590; PubMed=6255422;
Kawakami T., Takahashi N., Honjo T.;
Kawakami T., Takahashi N., Honjo T.;
"Complete nucleotide sequence of mouse immunoglobulin comparison with other immunoglobulin heavy chain genes Nucleic Acids Res. 8:3933-3945(1980).
                                                                                          [5]
REVISION (MOPC 104E).
MEDLINE=83075344; PubMed=6816276;
MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                 SEQUENCE (MYELOMA PROTEIN MOPC 104E).

MEDLINE=79223904; PubMed=111247;

MEDLY M.R., Sibley C.H., Fuhrman J.S., Schilling

"Amino acid sequence of a mouse immunoglobulin mu
Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=82051295; PubMed=6795090;

Goldberg G.I., Vanin E.F., Zrolka A.M.,

"Sequence of the gene for the constant 1

Balb/c mouse immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig mu chain C_region secreted form.
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                    Auffray C.,
                                                                                      Kehry M.R., Fuhrman
                                                                                                                                                                                                                                       "Nucleotide sequence of a cloned cDNA chain of mouse immunoglobulin.";
                                                                                                                                                                                                                                                                                                                    Gene 15:33-42(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                         Complete amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
              Event=Alternative
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12:77-86(1980)
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aplicing; Named isoforms=2;
differentiation, B lymphocytes
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Sciurognathi;
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PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
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PIR; A02166; MHMS
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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IsoId=P01872-1; Sequence=Displayed;
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Buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
178
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                                                | SPP----GSSP---SVQCR----SPR------GKNIQGG-----
                                                                                              ---PLIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                              TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF
YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST---
                                      VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKL
                                                                                                                    VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT------LRTGGKYLA
                                                                                                                                        VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
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10-OCT-2003 ()
Ig epsilon cha
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
                                                                                                       Bennich H.
(In) Bach
Immediate
                                                                                                                                                           epsilon
EMBO J.
                                                                                                                                                                    MEDLINE=84236029; PubMed=6234164; Flanagan J.G., Rabbitts T.H.; The sequence of a human immunoglobulin epsilon region gene, and evidence for three non-allelic EMBO J. 1:655-660(1982).
 "Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                          Kenten J.H., Molgaard H.V., Bell L.O., Gould H.J.;
                                                            SEQUENCE OF 1-40;
MEDLINE=83065234;
                                                                                                                          [5]
PRELIMINARY SEQUENCE (MYELOMA PR
                                                                                                                                                                                                                                                                                                                   MEDLINE=83001945; PubMed=6288268;
Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon
                                                                                                                                                                                                                                                                                                                                                                                  epsilon
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83168897; PubMed=6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of huebsilon chain cDNA.";
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                            pseudogene that lacks 1:1539-1544(1982).
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                                                                                     i.H., Johanse...

n.K. (eds.);
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New York (1978).
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1 chain C reg
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Primates;
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGC1; 4.
PROSITE; PS50835; IG LIKE; 4
PROSITE; PS00290; IG_MHC; 3.
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PDB; 11GE; 15-JUL-92.
PDB; 1FF5; 30-JAN-02.
PDB; 1G84; 16-MAY-01.
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Model of the Fc of immunoglobulin
Mol. Immunol. 23:1063-1075 (1986).
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19 mu chain C region secreted form.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata
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                                                                                                    PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                            QPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG
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                                                                                                                                        QPREPQVYTL----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT
                                                                                                                                                        GKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG
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Pred. No. 4.5e-16;
3; Mismatches 137;
 Craniata;
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of VHa2 allotype: comparisons with VHa1 and J. Immunol. 132:490-495(1984).
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MEDLINE=84088930; PubMed=6418803;
Bernstein K.E., Alexander C.B., Redd
"Complete sequence of a cloned cDNA."
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event-alter splicing; Named isoforms=2;
Event-alter splicing; Named isoforms=2;
Comment=During differentiation, B lymphocytes switch from
events of isoform Membrane-bound to isoform Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Membrane-bound
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P03988-1; Sequence=Displayed;
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VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--
                       ----SSRTV----RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
                                              NDRADSRRSLWDQGNFPLIIKNLK----
                                                                      ALTDGNLVAMG-----CLARDFLPSSVTFSWSFKNNSEI------
                                                                                             AATOGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
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encoding rabbit secreted mu-chain
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between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Use
entities requires a license agreement (See http
or send an email to license@isb-sib.ch).
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P20768;
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PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immuno
                                                                                                                                                                                 Pfam; PF00047; 1g; 4.
SMART; SM00407; IGc1; 3
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InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89232144; PubMed=2497033; Ishiguro H., Ichihara Y., Namikawa T., "Nucleotide sequence of Suncus murinus comparison with mouse and human mu gene FEBS Lett. 247:317-322(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
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Suncus murinus (House shrew) (Musk shrew).
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01-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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                                                                           QSLSRPKDVANDPPSVFVLPPAQEQLKLRESASITCLVKDFSPPD
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N-LINKED (GLCNAC.
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01-FEB-1996
15-JUL-1999
SEQUENCE FROM N.A.

MEDLINE=65297761; PubMed=2994005;

MCGuire K.L., Duncan W.R., Tucker P.W.;

"Phylogenetic conservation of immunoglobulin comparison of hamster and mouse Cmu genes.";

Nucleic Acids Res. 13:5611-5628(1985).
                                                                                                                                                       Mesocricetus auratus (Golden hamster)
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciuros
                                                                                                                   NCBI_TaxID=10036;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RA Stapleton M.J., Woell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Schernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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P09564;
D1-MAR-1989 (Rel. 10, Created)
D1-MAR-1989 (Rel. 10, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell antigen CD7 precursor (GP40) (T-cell leukemia
Haynes B.F.; "Characterization of the structure of the human
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Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes I
"Isolation and characterization of the genomic human
structural similarity with the murine Thy-L gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
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Mammalia;
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J. 6:3313-3316(1987).
                                                R.E.,
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                                                                                                             ning of the gene n antigen CD7."; 33:352-360(1991)
                                               PubMed=2479685;
e R.M., Dietz M.A.,
 of the surface topography numan CD7 molecule.";
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genomic human CD7
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GO:0005624; C:membrane fraction; TAS.
GO:0005886; C:plasma membrane; TAS.
GO:0004872; F:receptor activity; TAS.
GO:0006955; P:immune response; TAS.
GO:0042110; P:T-cell activation; TAS.
GO:0042110; P:T-cell activation; TAS.
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an email to license@isb-sib.ch).
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                                                                                                                                      Μ¥.
                                                         23; Mismatches 54;
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                                                                                                                                                                                                                               S-palmitoyl cysteine.
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
                                                                                                                                                                                                                                                                                                           FUNCTION. POTENTIAL.
                                                                               Score 316.5;
Pred. No. 1.0
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                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                             T-CELL ANTIGEN CD7
                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE
                                                                                                                                    EBBCE08279552108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor protein tyrosine kin. . .; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; Transmembrane;
Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Þ
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                                                                                                                                                                                                                                                                                                                                                  AA TANDEM REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE).
                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           (PROBABLE)
                                                           Indels
                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL SPACER
                                                                                               240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein,
                                                         49;
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                                                           Gaps
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RESULT 47
HVC2_HETFR
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Query Match
Best Local Similarity
                                                                                                                                                                      Immunoglobulin on NON TER 1 DOMAIN 108
                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991
                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVC2_HETFR P23085;
                                     SEQUENCE
                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain C region (Clone 12022) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                       SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.; "Complete structure and organization of immunoglobulin heavy chain constant region genes in a phylogenetically primitive vertebrate.", EMBO J. 7:1979-1988 (1988).

-i- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                      InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                             HSSP; P01842;
                                                                                                                                                                                                                                                                                                                        PIR; S00980; HVRKC2.
                                                                                                                                                                                                                                                                                                                                    EMBL; X07784; CAA30617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88328985; PubMed=3138109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7792;
                                                                                                                                                                                                                                                            Pfam; PF00047; ig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALARGLPGALAAQEVQQSPHCTTVPVGA-----SVNITCSTSGGLRGIYLRQLGPQPQ
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                                   1108
213
315
1166
200
245
275
275
374
411
415
415
425
AA;
                                                                                                                                                                                                                                                                                                             7FAB
                                                                                                                                                                                                          domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20, Last sequence update)
42, Last annotation update)
region (Clone 12022) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20, Created)
                                                 101
202
202
415
166
200
245
275
411
411
425
                                                                                                                                                                                                                                                                     Ig-like.
Ig_cl.
Ig_MHC.
                                     47904
11.5%;
25.4%;
                                                                                                                                                                                                             Immunoglobulin C region;
                                     MW.
                                               IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
IG-LIKE 4.
N-LINKED ((
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                     6E67A9C5BBF7AA7B
 312; DB 1;
No. 6.8e-13;
                                              438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512
                                                                                                                                                                                                             Glycoprotein; Repeat
                                     CRC64;
            Length 438;
                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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RESULT 48
MUC_CHICK
ID PO187
AC P0187
DT 21-JU
DT 01-FE
DT 15-JU
DT Gallu
OC Gallu
OC Gallu
OC Gallu
OC Gallu
OC Gallu
OC Gallu
CC Gallu
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01875;
21-JUL-1986
01-FEB-1991
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                          Weill J.-
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license sgreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 80-446 FROM N.A.

MEDLINE-33299221; PubMed-6310496;

Dahan A., Reynaud C.-A., Weill J.-C.;

"Nucleotide sequence of the constant
"Nucleotide bequence of the constant
chain immunoglobulin mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig mu chain C region.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
  HSSP; P01857; 1FC1.
InterPro; IPR007110;
InterPro; IPR003597;
                                                                          EMBL; X01613; CAA25762.1;
PIR; A02170; MHCH.
                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LEATVTLTCV---VSNAPYGVNVSW-----TOEKKPLKSEIAVQPGEDSDSVISTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 01, Created)
(Rel. 17, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11:5381-5389(1983)
Ig-like.
Ig_cl.
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                                                                             TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRDE
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                                  LINGNORLSVTCMAQGENPPHLFVRWMRNGEPLPQSQSVTSAFMAENPENESYVAYSVLGV
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                 This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are nouse by non-profit institutions as long as its conmodified and this statement is not removed. Usage by modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALC2 HUMAN P01877;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE (MYELOMA PROTEIN LAN).
MEDLINE=79180140; PubMed=286295;
Tsuzukida Y., Wang C.-C., Purnam F.W.;
"Structure of the A2m(1) allotype of human IgA --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flanagan J.G., Léfranc M.-P., Rabbitts T.H.; mechanisms of divergence and convergence of the alpha 2 constant region gene sequence cell 36:681-688(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                   MEDLINE=91054387; PubMed=2241915;
                                                                                                                                                                                                                                                                                   REVIEW.
                                                                                                                                                                                                                                                                                                                           molecule
                                                                                                                                                                                                                                                                                                                                                                                                          "Complete amino acid sequence of the alpha 2 heavy IgA2 immunoglobulin of the A2m (2) allotype."; Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Torano A., Putnam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=78137069; PubMed=416441;
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MEDLINE=84130179; PubMed=6421489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                       "The structure and function of human siochem. J. 271:285-296(1990).
                                                                                                                                                                                                                                                       Kerr M.A.;
                                                                                                                                                                                                                                                                                                            Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig alpha-2 chain
                                                                                                                  SUBUNIT: Monomeric or polymeric.
MISCELLANEOUS: The sequence of the A2m(1) allotype is shown
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                            FUNCTION: Ig alpha is the major immunoglobulin class in secretions. It may serve both to defend against local in and to prevent access of foreign antigens to the general
                                                                                                                                                                   immunologic system
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an email to license@isb-sib.ch).
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SMART; SM00407; IGC1; 2.

SMART; PS50835; IG_LIKE; 3

PROSITE; PS50835; IG_MIC; 2.

Immunoglobulin domain; Immun
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GO; GO:0003823; F:antigen b
GO; GO:0006955; P:immune re
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HSSP; P01810;
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                LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                     TTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPPC----
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IPR003006; Ig_MHC.
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V -> I (IN A2M(2) ALLOTYPE)
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F -> Y (IN A2M(2) ALLOTYPE)
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PIR; S01853; HVRKCS.
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the European Bioinformatics Institute. There are no restrict
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Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
Kokubu F., Hinds K., Litman R., Shamblott m.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain
constant region genes in a phylogenetically primitive vertebrate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus.
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01-NOV-1991 (Rel. 20, Last sequence upo
15-JUL-1999 (Rel. 38, Last annotation u
Ig heavy chain C region, secreted form
Heterodontus francisci (Horn shark).
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SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 4
PROSITE; PS00290; IG_MHC; 3.
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SMART; SM00407; IG
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  89
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                                                                                                                                                                                              Similarity
                                                                                                                           WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV-
RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing.
                                                                                                                                                                       Conservative
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                                                                                                                                                          Score 294; UB 1
Pred. No. 9.6e-17
65; Mismatches 1
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CH2.
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form (Clone
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                                                                                  SQLTITESEVGSSKIY-CEVR
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L outstation -
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              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ULT 52
RABIT
                                                                                                                             EMBL; X00353; CAA25100.1; -. PIR; A02174; AHRB. HSSP; P01857; 1FC1.
                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding IgA-g subclass alpha-chains.";

Nucleic Acids Res. 12:1657-1670(1984).

-i- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALC RABIT STANDARD; PRT; 299 AA P01879; PRT; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat Ig alpha chain C region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84144059; PubMed=6322114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knight K.L., Martens C.L., Stoklosa C.M., Scl
"Genes encoding alpha-heavy chains of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                It was isolated from a rabbit homozygous FOR A2, N8 F71, G75 heavy chain haplotype.
SIMILARITY: Contains 2 immunoglobulin-like domains.
                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                        immunologic system. MISCELLANEOUS: This
                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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   domain;
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                                                                                                                                                                                                                                                                                                                                                     This immunoglobulin belongs to the IgA-G d from a rabbit homozygous FOR A2, N80, DE
   Immunoglobulin C
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region; Repeat.
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Best Local
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Immunoglobulin on NON TER 1
DOMĀIN 40
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01-NOV-1991
10-OCT-2003
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DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=88328985, PubMed=3138109;
MEDILINE=88328985, PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain "Complete structure" and "Complete s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain C region (Clone 6125) (Fragment). Heterodontus francisci (Horn shark). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthye. Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus. NCBI_TaxID=7792;
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                Pfam; PF00047; ig;
SMART; SM00407; IGC
                                                                                                                                                                                                                                   PIR; S01851; HVRKC5.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                            modified and this statement
                                                                    SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                    EMBL; X07783; CAA30616.1;
                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 3 immunoglobulin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constant region genes in a phylogenetically primitive EMBO J. 7:1979-1988(1988).
                                                                                                                                                                 InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                               (nterPro; IPR007110;
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(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
ain C region (Clone 6125) (Fragment).
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                                              domain; Immunoglobulin C
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32256
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; Ig_cl.
; Ig_MHC.
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Pred. No. 6.9e-12;
2; Mismatches 106
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IG-LIKE 2.
2512FE3F62E9A223
  IG-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.
                                              region; Glycoprotein; Repeat
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Best Local S
Matches 101
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P23086;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain C region (Clone 6121) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Elasmobranchi; Galeomorphi; Heterodontoidea; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               LT 54
_HETFR
This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                    MEDLINE=88328985; PubMed=3138109; Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman "Complete structure and organization of immunoglobulin constant region genes in a phylogenetically primitive v EMBO J. 7:1979-1988(1988).
                                                                                                                                                                                                                          NCBI_TaxID=7792;
                                                                                                        EMBO J. 7:1979-1988(1988).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                         SSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLPPSRDELTKNQ-V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFTNTVYTCQVSHQAATQSRNI----TGSPDSSECNH------
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IG-LIKE 3
N-LINKED
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Pred. No. 2.3e-11;
9; Mismatches 155;
                                                                                                                                                                                                                                                      Heterodontoidea; Heterodontiformes;
                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
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in heavy chain
e vertebrate.";
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17, Creat 17, Last 42, Last region.

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update)

Created)

STANDARD;

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gorilla gorilla

(Lowland gorilla)

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RESULT
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DT 01
DT 11
DE 15
CGN 16
CGN 1
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Best Local
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PIR; S01852; HVRKC1.
HSSP; P01842; 7FAB.
TDD007110;
                                               1 GORGO
ALC1 GORGO
P20758;
01-FEB-1991
01-FEB-1991
10-OCT-2003
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CARBOHYD
SEQUENCE
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NON TER 1
DOMAIN 63
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 3
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                                                                                                                                                                                                                               IPLKIINRTVNKSSG
                                                                                                                                                                                                                                                                                                         REIFVKWTINDKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEA
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawamura S., Omoto K., Ueda S.;
"Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.";
Nucleic Acids Res. 17:6732-6732(1989).
-!- FUNCTION: Ig alpha is the major immunoglobulin class in body
secretions. It may serve both to defend against local infectio
and to prevent access of foreign antigens to the general
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SMART; SM00407; iGc1; 2.
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PROSITE; PS00290; iG_MHC; 1.
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SIMILARITY: Contains 3 immunoglobulin-like domains
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                                                                                                                                                                                                                                                                                                     Similarity
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                                       ED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVEGPPERDLCGCYSVSSVLP
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21-JUL-1986
the
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                 "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro. II. The amino acid sequence of the H-chain, alpha-type, subgroup II structure of the complete IgA-molecule.", Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
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01-FEB-1991 (Rel.
15-MAR-2004 (Rel.
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MEDLINE=76023781; PubMed=809331;
                                                                                                                                                                                                                                                                                                                                                                                                               IgAl protease, digestion, Fab and Fc fragments, and amino acid sequence of the alpha 1 heavy chain."; J. Biol. Chem. 254:2865-2874(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flanagan J.G., Lefranc M.-P., Rabbitts T.H.; "Mechanisms of divergence and convergence of the human "Mechanisms alpha 2 constant region gene sequences."; Cell 36:681-688(1984).
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Mammalia; Eutheria;
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                                             immunologic system.
SUBUNIT: Monomeric or polymeric.
SIMILARITY: Contains 3 immunoglobulin-like
                                                                                               chem. J. 271:285-296(1990).
FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infect
European
                                                                                                                                     structure and function of human
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                                                                                                                                                                                                                                                                                                                                                               Altevogt P., Ruban E.,
Bioinformatics
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GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGC1; 2.
PROSITE; PS00835; IG_LIKE; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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PDB; 1IGA; 15-JUN-
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                                                                                                                                92 FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF-----GLT------ANSDTHLLQG
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                                                                                                                                                              Similarity
RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPE
                                                                                           QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK 196
                HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                      IDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                          Q---LTL-----PATQCLA--GKSV-----
                                                                                                              FPLSCCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSS
                                     -DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-
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N-LINKED (GLCNAC...).

E -> D (in dbSNP:1407).

/FTId=VAR 014602.

TPS -> PST (IN REF. 2).

E -> B (IN REF. 3).

P -> S (IN REF. 3).

R -> H (IN REF. 3).

H -> R (IN REF. 3).

H -> R (IN REF. 3).
                                                                                                                                                   Score 277.5; I
Pred. No. 8.3e-
51; Mismatches
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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INTERCHAIN (WITH HEAVY CHAIN OF
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OR 123-182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52617; -; NOT_ANNOTATED_CDS. HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 18:527-523 (1990).
-!- MISCELLANEOUS: During differentiation, B lymphocytes switch freexpression of membrane-bound IgM to secretion of IgM. The mu chains of membrane and secreted IgM differ in their C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson M.R., Marcuz A., Middleton D., Warr G.W.;
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MEDLINE=90384824; PubMed=2119496;
MEDLINE=90384824; A., van Ginkel F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991
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SMART; SM00407; IG
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catfish, Ictalurus punctatus: an unusual the membrane form of the molecule.";
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15-MAR-2004 (Rel. 43, Last annotation of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mmunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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PROSITE; PS50835; IG_LIKE;
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Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SH9S-1) (Inhibitory receptor SH9S-1) (Signal-regulatory protein alpha-1) (Signal-latiory protein alpha-1) (Signal-latigen) (Brain Ig-like molecule with tyrosine-based activation motife) (Bit) (p84).
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P97797; O08907;
Q9WTN4;
Lagenaur C.F., Narayanan V.; "The murine P84 neural adhes phosphatase-binding protein
                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SEQUEN (ISOFORM 2), VARIANTS ALA-29; ARG-91; THR-96 N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
STRAIN-BALB/c; TISSUE-Brain, and Cerebellum; MEDLINE-98012243; PubMed-9348339; Comu S., Weng W., Olinsky S., Ishwad P., Mi 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamao T., Matozaki T., Amano K., Matsuda Y., Takahas
Fujioka Y., Kasuga M.;
"Mouse and human SHPS-1: molecular cloning of cDNAs
localization of genes.";
                                                                                                                                                                                                                                                                                                            Ohnishi
                                                                                                                                                                                                                                                                                                                                    MEDLINE=97230468; PubMed=9073522;
                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97223399; PubMed=9070220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                       (Bit)
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                                                                                                                                                                                                                                                                                                       H., Kubota M., Sano S.-I
                                                                                                                                                                                                                                                                                                                                                                                      SER-128;
                                                                                                                                                                                                                                                          t) maps to mouse chromosome 40:504-506(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biophys. Res. Commun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Rodentia;
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     adhesion molecule otein family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K., Matsuda Y., Takahashi N.,
                                                                                                                                                                                                                                                                                                                                                                                      ASN-224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                231:61-67(1997).
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                                                                         2.,
                             SHPS-1,
                                                                                                                                                                                   AND
                                                                               Hempel
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Murinae; Mus
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MEDLINE-20130295; PubMed=10662797;
Gresham H.D., Dale B.M., Potter J.W., Chang P.W., Vines C.M.,
Lowell C.A., Lagenaur C.F., Willman C.L.;
"Negative regulation of phagocytosis in murine macrophages by the
kinase family member, Fgr.";
J. Exp. Med. 191:515-528(2000).
-i- FUNCTION: Immunoglobulin-like cell surface receptor for CD47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), VARIANTS ALA-29; ARG-67; PRO-74; ALA-83; 86-TYR VAL-67; ILE-90; ARG-91; THR-96; ALA-114; ILE-918; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365; N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, INTERACT WITH PFPN6, AND TISSUE-FECTIFICITY.
STRAIN-C57BL/6; TISSUE-Fectal thymus; MEDLINE-98380500; PubMed-9712903;
                                                                                                                                                                                                                                                                                                          INTERACTION WITH CD47, AND TISSUE SPECIFICITY MEDLINE=99091586; PubMed=9872987;
Jiang P., Lagenaur C.F., Narayanan V.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Stofega M.R., Wang H., Ulli
"Growth hormone regulation
and association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehringer M.A., Thompson J., Conroy O., Xu
Beeson M., Gordon L., Bennett B., Johnson
"High-throughput sequence identification
"Within alcohol-related QTLs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-74; ALA-83; 86-T
ILE-118; SER-128; PR
STRAIN=ILS, and ISS;
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MEDLINE=20053880; PubMed=1058853;
Sano S.-I. Obnishi H., Kubota M.;
"Gene structure of mouse BIT/SHPS-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), VARIANTS ALA-29; PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365, AND ASP-365, AND ASP-365; AND ASP-365;
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                                                                                                                                                                     MEDLINE=20130295; Put
                                                                                                                                                                                                                                                                                  Jiang P., Lagenaur C.F., Nara
"Integrin-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-GLYCOSYLATION, PHOSPHORYLATION BY HORMONE, AND INTERACTIONS WITH JAK2 MEDLINE=98175985; PubMed=9507023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chuang W., Lagenaur C.F. "Central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, TISSUE SPECIFICITY, AND MEDLINE=90152134; PubMed=2303162;
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                                                                                                                                                                                                                                                                molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. 137:219-232(1990)
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docking
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                                                                                                                                                                                                                                          274:559-562(1999).
                                                                                                                                                                                                                                                                                                                                                                                                           273:7112-7117(1998)
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    translocation
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AND PTPN
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EMBL; D87967; E
EMBL; D87968; E
EMBL; D85785; E
EMBL; U89694; J
EMBL; AF072543
EMBL; AF072544
EMBL; AB024507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Names: Synonyms b, Small;
IsoId=P97797-3; Sequence=VSP_007031;
IsoId=P97797-3; Sequence=VSP_007031;
spinal cord, cerebellum and spleen, and at much lower levels in kidney, thymus, heart, lung and liver. Within the cerebellum, highly expressed throughout the molecular layer, and in synaptic glomeruli in the granule cell layer. Detected in neurons of the hippocampus and dentate gyrus, and in olfactory bulb. Not detected in Purkinje cells. Highly expressed in the plexiform layers, optic fiber layer and the outer segments of the photoreceptor layer in the retina. Highly expressed in macrophages. Isoform 3 is detected at very low levels in all tissues tested.

-i. DEVELOPMENUTAL STAGE: Highly expressed in the CNS of embryos from day 7 to 17.
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        EMBL,
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L; AF072543; AAC24886.1; AF072544; AAC24887.1; AF072544; AAC24887.1; AB024507; BAA89290.1; JOIN L; AB024501; BAA89290.1; JOIN L; AB024501; BAA89290.1; JOIN L; AB024503; BAA89290.1; JOIN L; AB024504; BAA89290.1; JOIN L; AB024505; BAA89290.1; JOIN L; AB024505; BAA89290.1; JOIN L; AB024505; BAA89290.1; JOIN L; AB024507; BAA89289.1; JOIN L; AB024507; BAA89289.1; JOIN L; AB024501; BAA89289.1; JOIN L; AB024501; BAA89289.1; JOIN L; AB024501; BAA89289.1; JOIN L; AB024503; BAA89289.1; JOIN L; AB024503; BAA89289.1; JOIN L; AB024503; BAA89289.1; JOIN L; AB024504; BAA89289.1; JOIN L; AB024505; BAA89289.1; JOIN L; AB024506; BAA89289.1; JOIN 
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PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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IsoId=P97797-1; Sequence=Displayed;
Name=2; Synonyms=a', Large;
IsoId=P97797-2; Sequence=VSP_007032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factors or insulin. Mediates negative regulation of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells (By similarity). SUBUNIT: Binds FTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds FTPN6. Binds GRB2 vitro. Binds FGR. Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds FYE2B (By similarity). SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPN11 and other binding partners from the cytosol to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment=Additional isoforms
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Best Local
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MGD; MGI:108563; Ptpnsl.

GO; GO:0008580; F:cytoskeletal regulator activity; IMP.

GO; GO:0045309; F:phosphoprotein amino acid binding; IP

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0007015; P:actin filament organization; IMP.

GO; GO:0007150; P:cell motility; IMP.

GO; GO:0007160; P:cell-matrix adhesion; IMP.
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EMBL; AF332080; AAK56108.1;
EMBL; Y10349; CAA71375.1; -
                                                                                           424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                     HITLDR--SPLRGIANLSNFIRVSPTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIWLE
MOTFPGNNATHNWNVFIGVGVACAL 384
                             ASALPAALAVISFLLGLGLGVACVL
                                                            LGLAHS
                                                                                          KSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTASALPDPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                                                                                                                                                                                                                     PAPIEKTISKAKGQPREPQVYTLPPS----RDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                SPRNITLKWFKDGQELHHLETTVNPSGKNVSYNISSTVRVV----LNSMDVHSKVICEVA
                                                                                                                                                                                                                                                                                EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                                                                                                                           ----PRVTNVSDATKRNNMDFSIRISNVTPEDAGTYYCVKFQ------
                                                                                                                                                                                                                                                                                                                                                                                                          LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPEKSVSVAAGDSTVLNCTLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                                                                                                         NGNVSRN--DTPKNLTKNTDGTYNYTSLFLVNSSAHREDVVFTCQVKHDQQPAITRNHTV
                                                                                                                                                     NGQPENNYKTTPPVL--DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYTQ
                                                                                                                                                                                                                                                                                                                                              PAPEPKSCDKTHTCPELLGGPSVFLF----PPK---PKDTLMISRTPEVTCVVVDVSH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                KGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTC----KSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%;
19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 199; DB 1;
; Pred. No. 1.4e-05;
63; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .:
                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VGQSRLLIYSFTGE---HF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SLLPVGPIK-----
                                                            ---SDQGS
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RESULT 60
SHS1_RAT
ID SHS1_RAT
ID SHS1 RAT
STANDARD; PRT; 509 AA.
AC P97710; 000951; 070426; Q9QWI5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence)
DT 10-OCT-2003 (Rel. 42, Last sequence)
DT 10-OCT-2003 (Rel. 42, Last sequence)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (Sirp-alpha-1) (Brain Ig-like molecule
DE with tyrosine-based activation motife) (Bit) (Macrophage fusion
DE receptor) (Macrophage membrane protein MFPI50).
GN PTPNS1 OR SHPS1 OR SIRP OR BIT OR MFR.
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OS Caukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158;
RP 174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 AND
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as docking protein and induces translocation of PTPN6,
PTPN11 and other binding partners from the cytosol to the
plasma membrane. Supports adhesion of cerebellar neurons, neurite
outgrowth and glial cell attachment. May play a key role in
intracellular signaling during synaptogenesis and in synaptic
function. Involved in the negative regulation of receptor tyrosine
kinase-coupled cellular responses induced by cell adhesion, growth
factors or insulin. Mediates negative regulation of phagocytosis,
mast cell activation and dendritic cells activation. CD47 binding
prevents maturation of immature dendritic cells. May play a role in
the release of nitric oxide by macrophages (By similarity).
SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
Binds FGR. Binds JAK2 irrespective of its phosphorylation status
and forms a stable complex. Binds SCAP1 and (BY SCAP12. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takada T., Matozaki T., Takeda H., Fukunaga K., Noguchi Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F., Kas "Roles of the complex formation of SHPS-1 with SHP-2 in insulin-stimulated mitogen-activated protein kinase acti J. Biol. Chem. 273:9234-9242(1998).
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Ullu E., V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98008865; PubMed=9344856; Ochi F., Matczaki T., Noguchi T., Fujioka Y., Yamao T., Takada T., Tudada M., Takeda H., Fukunaga K., Okabayashi Y., Kasuga M.; Tspidermal growth factor stimulates the tyrosine phosphorylation of SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing protein tyrosine phosphatase ", Biochem. Biophys. Res. Commun. 239:483-487(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPEC: STRAIN-WAG/R.ij; TISSUE-Alveolar macrophage; MEDLINE-98375871; PubMed-9712053; Adams S., van der Laan L.J.W., Vernon-Wilson Renardel de Lavalette C., Doepp E.A., Dijkstvan den Berg T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Signal-regulatory protein is selectively neuronal cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Fischer 344; TISSUE=Macrophage;
MEDLINE=98449911; PubMed=9774638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
419-429; 446-467 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE-Bra
MEDLINE-97415431; PubMed-9271230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N. PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing protein tyrosine phosphatase and cell adhesion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98204923; PubMed=9535915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYR-460; TYR-477 AND TYR-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION OF TYR-477 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION
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and forms a stable complex. resulting complex recruits !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161:1853-1859(1998)
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AND 496-506, N-GLYCOSYLATION,
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AND TISSUE
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Pfam; PF00047; ig; 3.

SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG\_LIKE;

PROSITE; PS00290; IG\_MHC; 1

Phosphorylation Transmembrane;

Immunoglobulin domain; SH3-binding;

InterPro; InterPro;

IPR007110; Ig-like. IPR003597; Ig\_c1. IPR003006; Ig\_MHC.

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EMBL; D85183; BAA12734.1; --
EMBL; D38468; BAA20368.1; --
EMBL; D62328; AAC68478.1; --
EMBL; AF055665; AAC18089.1;
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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d at lower levels in heart
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                                                                                                                                                                                                                                                                                                                                                                         TQADKSVSVAAGDSATLNCTVSSLTPVGPIKWFKGEGQNRSPIYSFIGGEHFPRITNVSD
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                                                                                                                                                                                                                                                                                                                                   -ATKRNNM----DFSICISNVTPEDAGTYYC-VKFOKGIVE-----PDTEIKSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
   STANDARD;
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4444055
44216
45055
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                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%;
21.2%;
                                                                     508
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                                                  384
                                                                                                                                                                                                                                                     -----YGFSPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KR -> MP (IN REF. 3; AA SEQUENCE).
G -> A (IN REF. 2).
D -> N (IN REF. 3; AA SEQUENCE).
N -> L (IN REF. 3; AA SEQUENCE).
N -> G (IN REF. 3; AA SEQUENCE).
G -> F (IN REF. 3; AA SEQUENCE).
E -> P (IN REF. 3; AA SEQUENCE).
NARE -> EGQN (IN REF. 3; AA SEQUENCE).
R -> E (IN REF. 3; AA SEQUENCE).
MISSING (IN REF. 3; AA SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINE PHOSPHORYLATION AND PTPN11
BINDING. ABOLISHES TYROSINE
PHOSPHORYLATION AND PTPN11 BINDING; WHEN
ASSOCIATED WITH F-436, F-460 AND F-477.
P -> L (IN REF. 4).
MISSING (IN REF. 4).
F -> I (IN REF. 3).
S -> C (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 192; DB 1;
Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION AND PTPN11 BINDING; WHEN ASSOCIATED WITH F-436, F-460 AND F-501. Y->F: STRONGLY REDUCES INSULIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y->F: STRONGLY REDUCES INSULIN-INDUCED TYROSINE PHOSPHORYLATION AND PTPN11 BINDING. ABOLISHES TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND PTPN11 BINDING; WHEN F-436, F-477 AND F-501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y->F: ABOLISHES TYROSINE
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5BE1FE0A4DD429F4
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 159;
  387
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                158;
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  "The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9P1W8; Q8WWA5; Q9NQK8;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Signal-regulatory protein beta-2 precursor (S
                                                                                                                                                                                                           TISSUE=Lung;
                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                            Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21036165; PubMed=11185750;
Ichigotani Y., Matsuda S., Machida K.,
Yamaki K., Hayakawa T., Hamaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NA sequence and comparative 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORM
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RA Deloukas P., Matthews L.H., Abhurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Huckle E., Hunt A.R., Hunt S.E., Jokosch K., Johnson C.M., Johnson D.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jokosch K., Johnson C.M., Johnson D.J.,
RA Kay M.P., Kimberley J.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Koepers J.,
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max.
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Keckwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rahas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holtey J., Helton E., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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"Molecular cloning of a novel human gene (S:
member of the SIRP/SHPS-1 protein family.";
J. Hum. Genet. 45:378-382(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SIRP-beta-2)
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Query Match
Best Local Sim
Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Igcl; 3.
SMART; SW00406; IGcl; 2.
SMART; SW00406; IGcl; 2.
SMART; SW00406; IGcl; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_MHC; FALSE
                                                                                                       CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB042624; BAA95692.1; -.
EMBL; AL138804; CAC00474.1; -.
EMBL; BC020629; AAL7_INIT.
Genew; HGNC:15757; SIRPB2.
                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Signal;
Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 605466; -.
GO:0007246; P:cell-cell signaling; TAS.
GO:0007242; P:intracellular signaling cascade; TAS.
GO:0008285; P:negative regulation of cell proliferation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 2 immunoglobulin-like C1-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in liver, and at very
brain, heart, lung, pancreas, kidney, placenta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Probable immunoglobulin-like cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9P1W8-2; Sequence=VSP_007027;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9P1W8-3; Sequence=VSP_007028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (soId=Q9P1W8-1; Sequence=Displayed;
6 PFRHLLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                      Similarity
                                                                                                                                                                                                           e splicing. 28 29 387 29 360 361 383 384 29 340 137 29 119 226 329 329 329 329 329 317 N. 33
                                   Conservative
                                                                                                                                                                              144
                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                360
                                                  7.0%;
                                                                                                           42495
                                                                                                             X
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALSE_NEG.
                                 56;
                                                                                                                        /FTId=VSP_007027.
Missing (In isoform ;
/FTId=VSP_007028.
A -> V (IN REF. 2).
L -> S (IN REF. 2).
                                                                                                                                                                                                                                                    N-LINKED
                                                    Score 188.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                  Missing
                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-REGULATORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                         F7F20C9F86E0E64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain;
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane
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                                                                                                                                                                                                                               ; DB 1;
1.5e-05;
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                                   Indels 173;
                                                                   Length
                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
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                                                                     387;
                                 Gaps
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                        PTGSALPDPQTASALPDPPAASALPAALAVISFLLG
                                                                                   QGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAP
                                                                                                                                               TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                                                                                                                  PADVGTYYCVKFRKGSPENVEFK--
                                                                                                                                                                                                                                                                                                                              LQDSGTWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSV-FLFPPKP
                                                                                                                                                                                                                                                                                                                                                                                        EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDVVLTCQVKHDG-----QLAVSKRLALEVTVHQKD--
                                                                                                                   AGNQVNVTCQVRKFYPQSLQLTWLENGNVCQRETASTLTENKDGTYNWTSWFLVNISDQR
                                                                                                                                                                            IRSTARVVLDPWDVRSQVICEVAHVTLQGDPLRGTANLSEAIRVPPTLEV-TQQPMR----
                                                                                                                                                                                                        VVSVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                       SAPVVLGPAARTTPEHTVSFTCESHGFSPRDITLKWFKNGNELSDFQTNVDPTGQSVAYS
                                                                                                                                                                                                                                                                   KDTLMIS----RTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP---LIIKNLKIEDSDTYICEVEDQK 115
-----QSSDATPGP--ASSL-TALLLIAVILG
                                                                                                                                                                                                                                                                                                                                                            ----GHFPRVTTVSDLTKRNNMDFSIRISSIT
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RESULT 62
SHS1BODT
ID SHS1
ID SHS1
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ID O04663
DT 10-00
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046631; 046632;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (MyD-1 antigen).

PTPNSI OR SHPSI OR SIRP OR MYD1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Brooke G.P., Parsons K.R., Howard C.J.;
"Cloning of two members of the SIRP alpha family of protein tyrosine phosphatase binding proteins in cattle that are expressed on monocyte and a subpopulation of dendritic cells and which mediate binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIS-120; 125-GLN;
ASP-203; ARG-261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Friesian; TISSUE=Peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND GLU-433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                          CD4 T cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                        as docking protein and induces translocation of PTPN6, PTPN11 and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, no outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synapt function. Involved in the negative regulation of
                                                                                                                                                                                                                                                                                                          FUNCTION: Immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                  J. Immunol. 28:1-11(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., AND VARIANTS SER-23; ALA-28; LEU-61; ARG-70; 127-GLY; 129-HIS; 132-VAL; ASN-145; VAL-153; LEU-302; LEU-316; ARG-337; ASN-367; LEU-422; P
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responses
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Repeat; Signal
Glycoprotein;
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SMART; SM00407; IGc1; 2.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Phosphorylated on tyrosine residues (By similarity). SIMILARITY: Contains 2 immunoglobulin-like C1-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binds JAK2 irrespective of its phosphorylation status ar stable complex. Binds SCAP1 and/or SCAP2. The resulting recruits FYB. Binds FGR and FYESE (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Highly expressed in spleen macrophag Detected in skin dendritic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dendritic cells and inhibits cytokine production by mature dendritic cells and inhibits cytokine production by mature dendritic cells (By similarity).

SUBUNIT: Binds PTPNI1 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.

Binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and forms a binds JAK2 irrespective of its phosphorylation status and binds
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P850835; IG_LIKE; 3.

P8508290; IG_MHC; FRALSE NEG.
; ES00290; Transmembrane; Tmmunoglobulin
Signal; Transmembrane; Tmmunoglobulin
Signal; Transmembrane; Polymorphism.
POTENTIAL.

POTENTIAL.
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IG-LIKE V-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
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SH2-BINDING
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TYPE SUBSTRATE 1.
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RESULT 63
LAC1_MOUSE
ID LAC1_MOUSE
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Matches 71
                                                                                       P01843;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Ig lambda-1 chain C region.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                             Selsing E., Mi
"Evolution of
                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                      MEDLINE-83014953; PubMed-6812053;
Selsing E., Miller J., Wilson R., Storb U.;
"Evolution of mousee immunoglobulin lambda g
Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              LTVSAKPSPPVLSGPTV
                                                                                                                                                                                  DODTGOTPGPNDSNWTS
                                                                                                                                                                                                 EAQDGEL----DGLWTT
                                                                                                                                                                                                                VFVENKDGTFNQTSWFLVNSSAHREAVVLTCQVEHDG-----QPAVSKNHTLEVSAPQK
                                                                                                                                                                                                                                PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCA
                                                                                                                                                                                                                                                                                              VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA--PIEKTISKA
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                                                                                                                                                                                                                                                              KGQPREPQVYTLPPSRDELT-----KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                              NELSASOTSVDPEDNIVSYSINSTTKVLLATGDVHSQVICEVAHVTLQGGPPL-----
                                                                                                                                                                                                                                                                                                                                                    PRGKNIQGGK-----TLSVSQLELQDSGTWTCTVLQNQKK--VEFKIDIVPCPAPEPK
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Pred. No. 6.3e
52; Mismatches
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79:4681-4685(1982).
                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                            PRT;
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ches 139;
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MEDLINE=81148806; PubMed=6259534;

SEQUENCE FROM N.A.

(MOPC 315)

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RESULT 64
VCA1_RAT
ID VCA1_RAT
AC P29534;
DT 01-APR-1993
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00582; AAA51636.1; -.
EMBL; J00587; AAB59672.1; -.
PIR; A93922; LIMS.
PDB; 1JNH; 06-FEB-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entitles requires a license agreement (Some send an email to license@isb-sib.ch).
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MEDLINE=71107854; PubMed=5276767;
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Gefter M.L., Baltimore D
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Somatic variants of murine immunoglobulin lambda light chains.";
Nature 298:380-382(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bothwell A.L.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ino acid sequences of two mouse immunoglobulin lambda chains."; C. Natl. Acad. Sci. U.S.A. 68:590-594(1971)

MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1 normal lambda-2 chain and 1 abnormal lambda-1 chain that is missing a large part of the V region. The C region sequence (shown here) appears completely normal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     here) appears completely normal.
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                     385
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                                                                                                                                                                                               l Similarity
37; Conserv
                                                                                                                                                        QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD
                                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                             QPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQ
                                                                                           SNNKYMASSYLTLTARAWERHSSYSCOVTHE---GHTVEKSLS
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104
19
56
75
81
81
85
  (Rel. 25, Created)
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                   8
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               domain; Immunoglobulin C region; 3D-structure.
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104
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                                                                                                                                                                                                                                                ET -> TE (IN REF. 4).

Q -> E (IN REF. 4).

MISSING (IN REF. 4).

HS -> SH (IN REF. 4).

S -> SS (IN REF. 4).

E -> Q (IN REF. 4).

M; A89F2BO9BCFCAO18 CRC64;
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                                                                                                                                                                                                            Score 177.5;
Pred. No. 4.4
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                                                                                                                                                                                                                                                                                                                                          INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                     IG-LIKE
                           PRT;
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the MOPC-315 plasmacytoma.";
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                                                                                                                                                                                                                                                                                                                               IN (WITH F
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                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                            HEAVY CHAIN).
                                                                                                                                                                                                                        Length 105;
                                                                                                                                                                                               Indels
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                                                                                           100
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PRINTS; PRO1472; ICAMVCAM1.
PRINTS; PRO1474; VCAM1.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 5
Immunoglobulin domain; Glyco
              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR00558; Ig c2.
InterPro; IPR003989; VCAM-1.
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VCAM1 OR VCAM-1.
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10-OCT-2003
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92181437; PubMed=1371918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 issp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and inflamed tissue. SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS0675; JS0675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P19320; 1VCA
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, Miyake K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
11 adhesion protein 1 precursor (V-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA42332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
               Chordata;
Rodentia;
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81246
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          IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 4
IG-LIKE C2-TYPE 5
IG-LIKE C2-TYPE 6
IG-LIKE C2-TYPE 7
IG-LIKE C3-TYPE 1
IG-LIKE C3-T
                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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VASCULAR CELL
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan
protein precursor (HSPG) (Perlecan) (PLC).
                                                                                                                                                 MUDLINE-92235084; PubMed=1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Tozzo R.V.; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Tozzo R.V.; "Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSPG2/perlecan). A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor."; J. Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92112994; PubMed=1730768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-OCT-1996 (Re
                                      MEDLINE=20553141;
                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Colon,
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"Human basement membrane heparan sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -kD protein containing multiple domains
density lipoprotein receptor, laminin,
ecules, and epidemmal growth factor.";
Cell Biol. 116:559-571(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPKIL--WSRQLKNGELQ-----
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       Davoine
22-4391 FROM N.A., AND VARIANT
53141; PubMed=11101850;
Davoine C.-S., Topaloglu H., Cat
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                                                                                                                                                                                                                                                                                                                                                                                                              Skin;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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   Cattolico
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DETCAEAQDGELDGLW
                                                                            TYR-1532
   L., Barral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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AND O-LINKED OLIGOSACCHARIDES.

-!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel syndrome (SJS1) [MIM:255800]; a rarre autosomal recessive disordaracterized by permanent myotonia (prolonged failure of must relaxation) and skeletal dysplasia, resulting in reduced statukyphoscoliosis, bowing of the diaphyses and irregular epiphyse -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
-!- SIMILARITY: Contains 3 laminin EGF-like domains.
-!- SIMILARITY: Contains 3 laminin IV domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 1 SEA domains.
                                                                                                                                                                                                                                                                                                                                                                  "Cloning of human heparan sulfate proteoglycan core assignment of the gene (HSPG2) to 1p36.1---p35 and a BamHI restriction fragment length polymorphism."
                                                                       between
                                                                                This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22660472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITE ASN-2121.
MEDLINE=22660472; PubMed=12754519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its promoter."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen I.R., Graessel S., Murc
"Structural characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-21 F
MEDLINE=94052171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kallunki P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fibrosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Heparan sulfate proteoglycan of human colon: partial cloning, cellular expression, and mapping of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92120660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91365376; PubMed=1679749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1016-1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSUE=Col
                                                       ween the Swiss Institute of Bioinfo
European Bioinformatics Institute
                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Found in the basement membranes.
PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL F
                                                                                                                                                                                                                                                                                                                   properties. It serves as an attachment substrate for cells. SUBUNIT: Purified perlecan has a strong tendency to aggregate dimers or stellate structures. It interacts with other basemen membrane components such as laminin, prolargin and collagen ty
                                                                                                                                                                                                                                                                                                          I۷.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arm of human chromosome ics 10:673-680(1991).
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F., Iozzo R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11:389-396(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52171; PubMed=8234307;
Graessel S., Murdoch A.I
characterization of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                890-1396 FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1685141;
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Lehmann-Horn
                                                        yright. It is produced through of Bioinformatics and the EM Institute. There are no restr
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1.";
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human
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                                                                                                                                                                                                                     failure of muscl
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                                                       restrictions
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EMBL; X62515; CAA44373.1; -.
EMBL; M85289; AAA52700.1; -.
EMBL; M85289; CAC18534.1; -.
EMBL; M64283; AAA52699.1; -.
EMBL; S76436; AAB21121.2; -.
EMBL; L22078; -; NOT ANNOTATED_CDS.
EMBL; L22078; A38096 A3809 A38096 A3809 A38096 A3809 A38096 A3809 A38096 A38096 
                                                                                                                                                                                                                                                                                                                                             SWART, SHOULD, SEA, I.

SMART, SMOOZOD; SEA, I.

PROSITE; PSO002; EGF 1; 9.

PROSITE; PSO1186; EGF 2; 6.

PROSITE; PS50026; EGF 3; 4.

PROSITE; PS50026; EGF 3; 4.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS50026; LAMININ TYPE EGF; 11

PROSITE; PS01249; LDLRA, I; 4.

PROSITE; PS01209; LDLRA, 2; 4.

PROSITE; PS50068; LDLRA, 2; 4.

PROSITE; PS50068; LDLRA, 2; 4.

PROSITE; PS50068; LDLRA, 2; 4.

PROSITE; PS50074; SEA; T.

Signal; Basement membrane; Proteoglyca Heparan sulfate; Laminin EGF-like domain; SIGNAL

SIGNAL

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POTENTIAL

SIGNAL

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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0261; LDLRECEPTOR.
PRODOM; PRO03031; LAMININ B; 3
SWART; SW00181; EGF; 15.
SWART; SW00180; EGF Lam; 12.
SWART; SW00409; IG; 22.
SWART; SW00409; IG; 21.
SWART; SW00406; IGC; 21.
SWART; SW00406; IGC; 7.
SWART; SW00406; IGV; 7.
SWART; SW00281; LAMB; 3.
SWART; SW00281; LAMB; 3.
SWART; SW00280; SEA; 1.
SWART; SW00280; SEA; 1.
      DOMAIN
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InterPro;
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n; PF000047; ig; 22.

n; PF00052; laminin_B; 3.

n; PF00053; laminin_EGF; 7.

n; PF00054; laminin_G; 3.

n; PF00057; ldl recept_a; 4.

n; PF01390; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      j ipr008985; ConA like_lec_gl.
j ipr000742; EGF 2.
j ipr0006209; EgF 2.
j ipr006210; IEGF.
j ipr00310; Ig-like.
j ipr003598; ig-c2.
j ipr003598; ig-c2.
j ipr003598; ig-c2.
j ipr003034; Laminin_B.
j ipr00034; Laminin_EGF.
j ipr002049; Laminin_G.
j ipr002049; Laminin_G.
j ipr002172; LDL_receptor_A.
j ipr00008: EGF. 4
      80
198
284
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367
405
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731
764
879
924
1126
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4391
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871
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1125
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EGF 2.
EGF_like.
IEGF.
                                                                                                                                                                                                                                                                                                                                 orane; Proteoglycan; Repeat; Glycoprotein;
nin EGF-like domain; Immunoglobulin domain
EGF-like domain; Disease mutation.
11
POTENTIAL.
11
BASEMENT MEMBRANE-SPECIFIC HEPARA
SULFATE PROTEOGLYCAN CORE PROTEIN.
SEA,
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE 1.
LAMININ EGF-LIKE 1 (N-TERMINAL).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (C-TERMINAL).
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PROTEOGLYCAN CORE PROTEIN.
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RESULT 66

LAC2 RAT

LAC2 RAT

TD TAC2 RAT

Ol-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Murinae; Ratt
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Best Local S
Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                          STPA
                                                                                                                                                                                                                   ALPA
                                                                                                                                                                                                                                                                                                               KGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC---
                                                                                                                                                                                                                                                                                                                                                                        KEYKCKVSNKALP---APIEKTISKAKGQP---REPQVYTLPPSRDELTKNQVSLTCLV-
                                                                                                                                                                                                                                                                                                                                                                                                         LDLNCVVPGQAH----AQVTWYKRG-----GSLPARHQTHGSQLRLHLVSPA-----DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGSSGTLEASVLVTIEPSSPGPIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVAEGQTLDLKC-VVPGQAHAQVTWHKRGGNLPARHQVHGPLLRLNQVSPADSGEYSCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLIIKNLKIEDSDTYICEVEDQK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGETLDLNCVVPGQAHAQVTWH------KRGGSL---PSHHQTRGSRLR
                                                                                                                                                                                                                                             NAYGVAQSVVNLSVHGPPTVSVLPEGPVWVKVGKAVTLECVSAGEPRSSARWT----RIS
                                                                                                                                                                                                                                                                                                 DGAAP--ISLEWKTRNQELEDNVHISP----
                                                                                                                                                                                                                                                                                                                                                    GEYVCRAASGPGPEQEASFTVTVPPSEGSSYRLRSPVISIDPPSSTVQQGQDASFKCLIH
                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQNQKKVEFKIDIV-----PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRT
                                                                                                                                                                                                                                                                       -----SVMHEALHNHYTQKSLSLSP-----GLQLDETCAEAQDGELDGLWTTDPPRAS
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AININ EGF-LIKE 7.

AMININ EGF-LIKE 8.

LAMININ EGF-LIKE 9 (N-TERMINAL).

LAMININ DOWALN IV 3 (DOWALN III C).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 7.

2340

IG-LIKE C2-TYPE 8.

2436

IG-LIKE C2-TYPE 9.

2533

IG-LIKE C2-TYPE 9.

1G-LIKE C2-TYPE 10.

7629

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 11.

775.5; DB 1; J

70.0064;

194;
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                    Rattus
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RESULT 67
             ACCOME BY ACCOME
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Matches 36
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TOTC
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21-JUL-1986 (Rel. 01, 0
21-JUL-1986 (Rel. 01, 1
10-OCT-2003 (Rel. 42, 1
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DISULFID
SEQUENCE
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NON TER
DOMAIN
6
                                                                                                                                                                                                                        SEQUENCE OF 1-162 (MYELOMA PROTEIN WAH).

MEDLINE-82082419; PubMed-6947220;

Putnam F.W., Takahashi N., Tetaert D., Debuire B.,

Putnam F.W., Takahashi N., Tetaert Constant region of

"Amino acid sequence of the first constant region of

hinge region of the delta heavy chain of human IgD

proc. Natl. Acad. Sci. U.S.A. 78:6168-6172(1981).
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                                                                                                   SEQUENCE OF 158-383 (MYELOMA PROT MEDLINE=81223768; PubMed=6787589; Lin L.-C., Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig delta chain C reg
IGHD.
Homo sapiens (Human)
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M22521;
HSSP; P01842;
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"Primary structure of the Fc region of human immunoglobulin implications for evolutionary origin and biological function Proc. Natl. Acad. Sci. U.S.A. 78:504-508(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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11318 MW;
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Pred. No. 9.8e
L7; Mismatches
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SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 2
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InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain."
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Shinoda T., Takahashi N., Takayasu T.
"Complete amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=82231401;
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                                                                                                                                       Similarity
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                          ATTRNTGRGGEEKKKEKEEGEERETKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFT
                                                           STPLQQWRQG-EYKCVVQHTASKSKKEIFRWPESPKAQASSVPTAQPQAEGSLAKATTAP
                                                                                            PKD----NSPVVLACLI-TGYHPTSVTVTWYM-GTQSQPQRTFPEIQRRDSYYMTSSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Contains 3 immunoglobulin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                            n immunoglobulin D.";
Res. Commun. 97:635-641(1980)
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PubMed=7092891;
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; Ig_MHC.
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Pred. No. 0.000
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INTERCHAIN
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(GLCNAC. . .).
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of a human
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                                          VYTLPPSRDEL-TKNQVSLT
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Shimizu
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CD22_HUMAN
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                                                                                                                                                                                                             SEQUENCE OF 13-137; 139-239; 241-328 AND 418-502 FRO VARIANTS THR-34; GLU-152; LYS-203; GLY-664; CYS-669 MEDLINE=99180618; PubMed=10079291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD22_HUMAN STANDARD; PRT; 847 AA.
P20273; O95699; O95701; O95702; O95703; Q01665; Q92872; Q92873;
Q9UQA7; Q9UQA8; Q9UQA9; Q9UQA9; Q9YZA6;
01-FEB-1991 (Rel. 17, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
B-cell receptor CD22 precursor (Leu-14) (B-lymphocyte cell adhesion molecule) (BL-CAM) (Siglec-2).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS CD22-ALPHA AND CD22-BETA).
Lamerdin J.E., McCready P., Adamson A.W., Burkhart-Schultz
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J.,
Bruce R., Quan G., Montgomery M., Ow D.,
INTERACTION WITH I MEDLINE=95343349;
                                                                  MEDLINE=93216636; PubMed=8463235;
Powell L.D., Sgroi D., Sjoberg E.R., Stamenkovic I., Varki A.;
"Natural ligands of the B cell adhesion molecule CD22 beta carry
N-linked oligosaccharides with alpha-2,6-linked sialic acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS MEDLINE-93267103; PubMed-849)
                                                                                                                            SIALIC ACID BINDING
                                                                                                                                                                                Hatta Y., Tsuchiya N.,
Tokunaga K.;
                                                                                                                                                                                                                                                                                                   Stamenkovic I.,
                                                                                                                                                                                                                                                                                                                MEDLINE-90231465;
                                                        required
                                                                                                                                                                                                                                                                                       The B-cell
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                          mmunogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions.
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                                                                                                                                                                                                                                                                       -cell antigen CD22 mediates monocyte and 345:74-77 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          structure and chromosomal ol. 150:5013-5024(1993).
                                        for recognition.";
Chem. 268:7019-7027(1993)
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                                                                                                                                                                                                                                                                                                                                                           A., Olsen A.O., (AUG-1996) to t
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                                                                                                                                                         49:280-286(1999).
                                                                                                                                                                      of the gene variations
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             PTPN6
 PubMed=7618087;
                                                                                                                                                                                                                                                                                                                  PubMed=1691828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                               Matsushita M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E., Menniger J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein CD22: a mediator
                                                                                                                                                                                                 Shiota
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                                                                                                                                                                      human
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                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                    erythrocyte adhesion.";
                                                                                                                                                                       CD22.";
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669 AND ASP-745
                                                                                                                                                                                                 Hagiwara
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the localization of B-cell interactions. May be involved in the localization of B-cells in lymphoid tissues. Binds sialylated glycoproteins; one of which is CD45. Preferentially binds to alpha2, -linked sialic acid. The sialic acid recognition site can be masked by cis interactions with sialic acids on the same cell surface. Upon ligand induced tyrosine phosphorylation in the immune response seems to be involved in regulation of B cell antigen receptor signaling. Plays a role in positive regulation through interaction with Src family tyrosine kinases and may also act as an inhibitory receptor by recruiting cytoplasmic phosphatases via their SH2 domains that block signal transduction through dephosphorylation of signaling molecules.

1. SUBUNIT: Predominantly monomer of isoform CD22-beta. Also found as heterodimer of isoform CD22-beta and a shorter isoform. Interacts with proper cells is soform CD22-beta and a shorter isoform.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Law C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96257803; PubMed=8647200;
Tuscano J.M., Engel P., Tedder T.F., Agar
"Involvement of p728yk kinase, p53/56lyn
inositol-3 kinase in signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphatase SHP.";
Science 269:242-244(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas M.L., Fearon D.T.;
"A role in B cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Annu. Rev. Immunol. 15:481-504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen receptor signaling.";
Annu. Rev. Immunol. 15:481-504(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fischer B.H., Clark E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH PTPN6; SYK AND F
MEDLINE=96195207; PubMed=8627166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ant igen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doody G.M., Justement L.B., Thomas M.L., Fearon D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CD22 associates with protein tyrosine phosphatase phospholipase C-gamma(1) upon B cell activation."; I. Exp. Med. 183:547-560(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97288746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH LYN; SYK AND
                                          PTM: Phosphorylated on tyrosine residues by LYN (I SIMILARITY: Belongs to the immunoglobulin superfan (stalic acid binding Ig-like lectin) family.

SIMILARITY: Contains 6 immunoglobulin-like C2-type SIMILARITY: Contains 1 immunoglobulin-like V-type CAUTION: Ref. 4 sequence differs from that shown du frameshift in position 806.

DATABASE: NAME-PROW: NOTE-CD guide CD22 entry;
                                                                                                                                                                                                       Name=CD22-alpha;
IsoId=P20273-2; Sequence=VSP_002531;
TISSUE SPECIFICITY: B lymphocytes.

TISSUE SPECIFICITY: B lymphocytes.

DOMAIN: Contains 4 copies of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPM6/SHP-1.

PTM: Phosphorylated both on threonine/serine and tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                      with PTPN6/SHP-1, LYN, SYK, PIK3R1/PIK3R2 and PLCG1 upon phosphorylation. Interacts with GRB2, INPPSD and SHC1 upo phosphorylation (By similarity). May form a complex with INPPSD/SHIP, GRB2 and SHC1.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                      Name=CD22-beta;
                      residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                        IsoId=P20273-1;
                                                                                                                                                                                                                                                                                                                                                                                                       Comment=Additional isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD22. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26:1246-1252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9143697;
ano J., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.P., Chandran K.A.,
                                                                                                                                                                                                                                                                                                                                                                    Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rwal A., Kehrl J.H.;
kinase and phosphatidyl
via the human B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                                                                                                                                                                                                                                                                           exist;
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                                                                                                                        domains
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collaboration

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á
                                                     Matches
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X59350; CAA42006.1; -.
EMBL; U62631; AAB06449.1; -.
EMBL; U62631; AAB06449.1; -.
EMBL; X52785; CAA436988.1; ALT FR.
EMBL; AB012996; BAA36565.1; -.
EMBL; AB012997; BAA36566.1; -.
EMBL; AB012999; BAA36567.1; -.
EMBL; AB012999; BAA36567.1; -.
EMBL; AB013000; BAA36569.1; -.
EMBL; AB013000; BAA36573.1; -.
EMBL; AB013004; BAA36573.1; -.
EMBL; AB013004; BAA36573.1; -.
EMBL; AB013006; BAA36575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 6.
SMART; SM00408; IGc2; 4.
PR0SITE; PS50835; IG LIKE; 6.
Cell adhesion; Lectin; Antigen
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                         mmunoglobulin
32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN 91
                 95;
                Conservative
                                                                                                                                                          842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB06449.1; -...
CAA36988.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                        domain;
                                                                              842
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                         6.2%;
                                                                                                                                                                                                                                                                                                                                                                                      Antigen; Transmembrane; Signal; Glycoprotein; Repeat; Phosphorylation; Alternative splicing;
               70;
                                                                                                                                                                                                                                   IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
ITIM MOTIF 1.
ITIM MOTIF 2.
ITIM MOTIF 3.
ITIM MOTIF 4.
                                                                                    PHOSPHORYLATION
(INVOLVED IN BINDING T
(BY SIMILARITY).
PHOSPHORYLATION
(INVOLVED IN BINDING T
(BY SIMILARITY).
                                                                                                                                                                  ITIM MOTIF 4.
BY SIMILARITY.
               Score 167; DB 1; I
Pred. No. 0.0028;
0; Mismatches 154;
                                                (INVOLVED IN BINDING TO SYK, PLCG2 AND PIK3R1/PIK3R2) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     B-CELL RECEPTOR CD22.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                        PHOSPHORYLATION (INVOLVED IN BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                Length 847;
               Indels 130;
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                                                                                              SYK)
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               Gaps
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A., Chen Z., Sures roteins that inhib -186(1997).  N.A. 449; PubMed=1178005 atthews L.H., Ashu rides G., Almeida low K.F., Batee K. Bird C.P., Blakey L. Butler A. Clamp M., Clark G. Ey V.E., Collier R. ville G.J., Deadma yille G.J., Deadma Griffiths C., Grif rley J.L., Heath P t A.R., Hunt S.E., erley J.M., Hand S.E., erley J.M., Hand S.E., trin S.L., McConna stry D., Moore M.J.	418 HNHYTOKSISLSPGLQLDETC 438  418 HNHYTOKSISLSPGLQLDETC 438	

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
   modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Whittaker P., Willey D.L., Beck S., Beck S., Walling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomasello E., Cant C., Buehring H.-J., Vely F., Andre P., Seiffert M Ullrich A., Vivler E., "Resociation of signal-regulatory proteins beta with KARAP/DAP-12."; Eur. J. Immunol. 30:2147-2156(2000).
                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11169422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257;
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                                                                                                                                                                   PTM: N-glycosylated.
SIMILARITY: Contains 2 immunoglobulin-like C1-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                   ween the Swiss Institute of Bioinf.
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Interacts with TYROBP. This interaction recruitment of SYK.
                                                                                                                                                                                                                                                                               TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative
                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ER
                                                                                                                                                                                                                                                                      IsoId=000241-2; Sequence=VSP_007026;
Note=No experimental confirmation available;
SSUE SPECIFICITY: Detected in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                               IsoId=000241-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VA sequence and comparative analysis of human chromosome 20.", 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parker A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12477932;
Feingold E.A., Grouse L.H.,
                            institutions as
                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing; Named isoforms=2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patel R.,
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removed.
                         There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                         dendritic
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                                                                                                                                                                                                            domains.
   and
                                                                                         EMBL
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InterPro; IPR003597; Ig_cl.
Pfam; PF00047; ig; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y10376; CAA71404.1; ---
EMBL; AL049634; CAB46661.2; ---
EMBL; AL13804; CAC17540.1; ---
EMBL; BC025286; AAH25286.1; ---
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Signal; Transmembrane; Immunoglobulin Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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; SM00407; IGc1; 2.
TE; PS50835; IG_LIKE;
                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                    82;
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                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                             GOSLITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKV
QQAVSKSYALEI---
                    QKSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALP
                                        QLTWLENGNVSRTETASTLIENKDGTYNWMSWLLVNTCAHRDDVVLTCQVEHDG
                                                            AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                                                                                CEMAHITLQGDPLRGTANLSEAIRVPPTLEV-TQQPMRAE----NQANVTCQVSNFYPRGL
                                                                                                    CKVSNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
                                                                                                                          GFSPRDITLKWFKNGNELSDFQTNVDPAGDSVSYSIHSTARVVLTRGDVHSQVI-----
                                                                                                                                            --EDPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                                                                                                                  EFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                          GAGRELIYNQKEGHFPRVTTVSELTKRNNLDFSISISNITPADAGTYYCVKFRKGSPDDV
                                                                                                                                                                                                                                                    Conservative
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SAHQKEHGSDITHEPALAPTAP
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Missing (in isoform 2
/FIId-VSp 007026.
R -> H (IN REF 2) CA
D -> N (IN REF 1).
                                                                                                                                                                                                                                                             Score 166.5,
Pred. No. 0.
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A (IN REF.
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                                                             422
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RESULT 70 UN89\_CAEEI ID UN89 AC 00176

CAEEL

UN89 CAEEL 001761; Q17362

STANDARD;

PRT;

6632

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DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Muscle M-line assembly protein unc-89 (Uncoor
UNC-99 OR CO9DL.1.
S Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rh:
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an c -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.

C -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.

C -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.

C -!- SIMILARITY: Contains 1 PH domain.

C -!- SIMILARITY: Contains 5 RCSD domains.
WormPep; C09D11; CE30426.
InterPro; IPR003957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003961; Ig-like.
InterPro; IPR003598; Ig-2.
InterPro; IPR003598; Ig-2.
InterPro; IPR003598; RCSD.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR0010219; RhoGEF.
InterPro; IPR001452; SH3.
Pfam; PF00041; fn3; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00161; RNOGEF; 1.
SMART; SM00408; IGC2; 23.
SMART; SM00325; RhoGEF; 1.
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[2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R
Submitted (MAY-1997) to
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U33058; AAB01
EMBL; AF003131; AAI
PDB; 1FHO; 20-DEC-(
WOrmPep; C09D1.1; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by modified entities
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STRAIN-Bristol N2;
MEDLINE-96180278; PubMed-8603916;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
"The Caenorhabditis elegans gene unc-89, required assembly, encodes a giant modular protein composed transduction domains.";
J. Cell Biol. 132:835-848(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         JU3131; AAB54132.2; -..., 20-DEC-00.
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y protein unc-89 (Uncoordinated
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          ^{9}
  PROSITE; PS50002; SH3; 1.

JONAIN INTERPRETATION IN
    RCSD 1.

RCSD 2.

RCSD 3.

RCSD 4.

RCSD 4.

RCSD 5.

IG-LIKE C2-TYPE 8.

IG-LIKE C2-TYPE 10.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 20.

IG-LIKE C2-TYPE 21.

IG-LIKE C2-TYPE 21.

IG-LIKE C2-TYPE 22.

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IG-LIKE C2-TYPE 23.

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IG-LIKE C2-TYPE 33.

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IG-LIKE C2-TYPE 34.

IG-LIKE C2-TYPE 44.

IG-LIKE C2-TYPE 45.

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IG-LIKE C2-TYPE 46.

IG-LIKE C2-TYPE 47.

IG-LIKE C2-TYPE 47.

IG-LIKE C2-TYPE 48.

IG-LIKE C2-TYPE 49.

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                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
   SEQUENCE FROM N.A. MEDLINE=83014953; PubMed=6812053;
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Rodentia;
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AKA -> PKP (IN REF. 1).

E -> G (IN REF. 1).

E -> G (IN REF. 1).

A -> PKP (IN REF. 1).

G -> A (IN REF. 1).

K -> N (IN REF. 1).

K -> FKP (IN REF. 1).

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Pred. No. 0.05
59; Mismatches
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POTENTIAL.
                                                                                                                                                Craniata; Veri
Sciurognathi;
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                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                    Muridae;
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RRROCCOSCEDE

protein precursor HSPG2.

Basement

Mus musculus (Mouse)

Eukaryota; Mammalia;

; Metazoa; Chordata; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

NCBI\_TaxID=10090;

SEQUENCE FROM N.A. TISSUE=Melanoma;

01-NOV-1995 (Rel. 01-NOV-1995 (Rel. 10-OCT-2003 (Rel.

32, Created)
32, Last sequence update)
42, Last annotation update)
specific heparan sulfate pr
(HSPG) (Perlecan) (PLC).

proteoglycan

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RESULT 72
PGBM_MOUSE
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Best Local S
Matches 35
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NON TER 1
DOMĀIN 6
DISULFID 27
DISULFID 103
SEQUENCE 104
                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PGBM_MOUSE
Q05793;
                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breyer R.M., Sauer R.T., Eisen H.N.; "The variable region of mouse lambda-3 chains."; ICN UCLA Symp. Mol. Cell. Biol. 20:105-110(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selsing E., Miller J., Wilson R., & "Evolution of mouse immunoglobulin Proc. Natl. Acad. Sci. U.S.A. 79:46 [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B93922; L3MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00585; AAB59670.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-18 (MYELOMA PROTEIN CBPC-49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=81223782; PubMed=6165998;
Azuma T., Steiner L.A., Eisen H.N.;
"Identification of a third type of lambda light
                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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roc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
                                                                                                         386
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                                                                                                                                                                                                      Similarity
                                                                                                                                                  QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                        DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                    QPKSTPTLTMFPPSPEELQENKATLVCLISNFSPSGVTVAWKANGTPITQGVDTSNPTKE
                                                                                DNKYMASSFLHLTSDQWRSHNSFTCQVTHE---GDTVEKSLS
                                                                                                                                                                                                                                                                                                                                                                           IPR007110; Ig-like.
IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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27
103
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                                                                                                                                                                                                                                           AΑ;
                                                                                                                                                                                                                                                                                                             domain; Immunoglobulin
               STANDARD;
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11371 MW;
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                                                                                                                                                                                      Score 163; DB
Pred. No. 0.00
16; Mismatches
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                                                                                                                                                                                                                                                                                    IG-LIKE
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79:4681-4685(1982).
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               3707
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                                                                                                                                                                                                                                                                                                             region
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EMBL; J04054; AAA39911.1; -.
EMBL; J04054; AAA39999.1; -.
PIR; S18252; S18252.
PBB; 1GL4; 28-NOV-01.
MGD; MG1:96257; HS9G2.
GO:00005604; C:basement membrar.
GO; GO:0005104; P:protein localiza.
InterPro; IPR000742; EGF 2:
InterPro; IPR000742; EGF 2:
InterPro; IPR0007100; ISGF-like.
InterPro; IPR0007100; ISGF-like.
InterPro; IPR0003598; IG-C2;
IPR0003598; IG-C2;
IPR0003598; IG-C3;
IPR0001791; Laminin_G.
IPR0001791; Laminin_G.
IPR0001791; LDL_receptor_A.
Pro; IPR000082; SEA_domain.
PF000008; EGF; 4.
PF0000047; IG: IF
                                                           Pfam; PF0000B; EGF; 4.
Pfam; PF000047; ig; 15.
Pfam; PF00052; laminin_B; 3.
Pfam; PF00053; laminin_EGF; 7.
Pfam; PF00054; laminin_G; 3.
Pfam; PF00057; ldl_recept_a; 4.
Pfam; PF01390; SEA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Noonan D.M., Horigan
Yamada Y., Hassell J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 940-1
MEDLINE=89034110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A criain, low density lipoprotein-receptor, and the neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinformatic
European Bioinformatics Institute. Ther
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send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: Contains 4 LDL-receptor class A domains.
SIMILARITY: Contains 11 laminin EGF-like domains.
SIMILARITY: Contains 3 laminin IV domains.
SIMILARITY: Contains 3 laminin IV domains.
SIMILARITY: Contains 15 immunoglobulin-like C2-type
SIMILARITY: Contains 3 laminin G-like domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 SEA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells. SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Extracellular. TISSUE SPECIFICITY: Found in the bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane components such as laminin, prolargin and collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
; PR00261; LDLRECEPTOR.
; PD003031; Laminin B;
SM00180; EGF Lam; 7.
SM00408; IGc2; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UE SPECIFICITY: Found in the basement membranes CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.A., Ledbetter S.R., R.;
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like_lec_gl.
                                                                                                                                                                                                                                                                                                                                                    membrane; IDA.
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SMART; SM00281; LamB; 3.

SMART; SM00282; LamG; 3.

SMART; SM00192; LDLa; 4.

SMART; SM00192; LDLa; 1.

SMART; SM00192; EGF 1; 8.

PROSITE; PS00022; EGF 2; 5.

PROSITE; PS50026; EGF 3; 4.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS50026; LAMININ TYPE EGF; 11

PROSITE; PS01248; LAMININ TYPE EGF; 11

PROSITE; PS01024; SEA; 1.

PROSITE; PS50068; LDLRA 1; 4.

PROSITE; PS50024; SEA; 1.
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Laminin EGF-like domain; Immunoglobulin domain;
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IN BGF-LIKE 1 (N-TERMINAL).

IN DOMAIN IV 1 (DOMAIN III A).

IN EGF-LIKE 1 (C-TERMINAL).

IN EGF-LIKE 3.

IN EGF-LIKE 3.

IN EGF-LIKE 4 (INCOMPLETE).

IN DOMAIN IV 2 (NO-TERMINAL).

IN DOMAIN IV 2 (NO-TERMINAL).

IN DOMAIN IV 2 (NO-TERMINAL).

IN EGF-LIKE 5.

IN EGF-LIKE 6.

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 9 (N-TERMINAL).

IN EGF-LIKE 10.

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                                       MP--IKVEWKIRDQELEDNVHISP-----NGSITTIVAPGPATMEPTACVASNVYGMAQS
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  VMHEALHNHYTQKSLSLSP-----GLQLDETCAEAQDGELDGLWT
                                                                               YPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLY---SKLTVDKSRWQQGNVFSC--S
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley N.C., Shevchenko Y., Bouffard G.G.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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01-APR-1990 (Rel. 1
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"Genomic structure of the human Ig lambda 1 gene suggests that it be expressed as an Ig lambda 14.1-like protein or as a canonical E cell Ig lambda light chain: implications for Ig lambda gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in pre-B cells and may encode the huma omega light-chain protein."; proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989)
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MEDLINE=89315835; PubMed=2501791;
Rvans R.J., Stafford-Hollis
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01-APR-1990 (Rel. 14, Last sequence update)
11-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
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Evans R.J., Hollis G.F.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; M34513; AAA36096.1; --
EMBL; M34511; AAA36096.1; JOINED.
EMBL; M34512; AAA36096.1; JOINED.
EMBL; M34512; AAA36096.1; JOINED.
EMBL; BC012293; AAH12293.1; --
PIR; A33911; A33911
HSSP; P01842; 7FAB.
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MEDIINE-83014953; PubMed=6812053;

MEDIINE-83014953; PubMed=6812053;

Selsing E., Miller J., Wilson R., Storb U.;

"Evolution of mouse immunoglobulin lambda genes.";

Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen;
SIGNAL
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MEDLINE=82220143;
                                                                Nucleic
                                                                               "Nucleotide sequence of a chromosomal immunoglobulin gene of mouse.";
                                                                                                                           MEDLINE=82274221; Publ
Wu G.E., Govindji N.,
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Creator)
21-JUL-1986 (Rel. 01, Last of 10-OCT-2003 (Rel. 42, Last of 10-DCT-2003) (Rel. 42, Last of 10-DCT-2003)
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SMART; SM00407; IGc1; 1.
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                      SEQUENCE
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 146770; ... GO:0016020; C:membrane; NAS. GO:0003793; F:defense/immunity GO:0006955; P:immune response;
                                                                                                                                                                                                                                                                                                                                           _TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385
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                                                                Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                      FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNNKYAASSYLSLTPEQWRSRRSYSCQVMHE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPKATPSVTLFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGTPITQGVEMTTPSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50835; IG_LIKE; 1. PS00290; IG_MHC; 1.
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email to license@isb-sib.ch).
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97
                   N.A.
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PubMed=6283385;
                                                                                                                                             PubMed=6287422;
                                                                10:3831-3843(1982)
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108
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                   (MOPC
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                                                                                                                           Hozumi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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IMMUNOGLOBULIN LAMBDA-LIKE P
J REGION (BY SIMILARITY TO L
LICHT-CHAIN).

C REGION (BY SIMILARITY TO L
LICHT-CHAIN).
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 on update)
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                                                                                                       rearranged lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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RESULT 75
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Best Local
                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ h
                                                                                                                                        HB2D
                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
                                                       Sus scrofa (Pig)
                                                                   precursor.
                                                                                                                           P15983;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
use by non-profit institutions as greates as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00595;
PIR; C93922; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a third type of lambda light chain immunoglobulins.";
Proc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azuma T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 66-104 (MOPC 315), AI MEDLINE=81223782; PubMed=6165998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry
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"Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dugan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=74048693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOPC-315)."
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                                                                                                                                                                                                                                                                                                                                                                                               mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                          l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Steiner L.A., Eisen H.
                                                                                                                                                                                                                      DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
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                                                                                                                                                                                               GNKFMASSFLHLTSDOWRSHNSFTCOVTHE---GDTVEKSLS
                                                                                                                                                                                                                                                                 QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                            QPKSTPTLTVFPPSSEELKENKATLVCLISNFSPSGVTVAWKANGTPITQGVDTSNPTKE
                                                                                                                                                                                                                                                                                                                                        104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradshaw R.A., Simms E sequence of the light
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               domain;
                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                        11254 MW;
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; Ig_cl.
; Ig_MHC.
                                                                                                                                                                                                                                                                                                   6.0%;
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                      Score 161;
Pred. No. 0
                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE
                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                           Mismatches
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chain of a mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              It is produced through a collaboration informatics and the EMBL outstation -
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Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=9823;

Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;

Euteleostomi Sus.

SEQUENCE

FROM N.A.

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RESULT
VCA1_HU
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                                                              01-NOV-1990 (Rel. 16, La
01-NOV-1990 (Rel. 16, La
10-OCT-2003 (Rel. 42, La
Vascular cell adhesion p
(INCAM-100).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003353; MHC_II_beta.
Pfam; PF00047; Ig; 1.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
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DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                           VCA1 HUMAN
P19320;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SP
PROSITE;
PROSITE;
                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a copyrender the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gustafsson K.,
Sachs D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Class II genes of ministure swine. IV expression of two allelic class II DQB J. Immunol. 145:1946-1951(1990).
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90361905; PubMed=2391424;
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                                                       VCAM1 OR L1CAM
                                           lomo sapiens
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E; PS50835; IG_LIKE; 1.
E; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                      SKAKG----QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN-NYK
                                                                                                                                                                                                                                                                                                                    WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                                                                                                                                       TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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                                                                                                                                                                                                                                                                                              WSVDRY-IYNQEEFLREDSDMGEYRAVTPLGRPDADYLNGQKEALEQKRAELDTVCKHNY
                                                                                                                                                                                                  STPLIRNGD----WTYQVLVMLEMNLQRGDVYTCRVEHSSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR007110;
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48
258
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(Rel. 16, Last sequence update)
(Rel. 42, Last annotation update)
(ladhesion protein 1 precursor (V
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                                            (Human)
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                                                                                                                                        STANDARD;
                    Chordata;
Primates;
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217
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X
                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                        Score 161; DB 1; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQ HAPLOTYPE D BETA CI
EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLA CLASS II HISTOCOMPATIBILITY DQ HAPLOTYPE D BETA CHAIN.
                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                              (V-CAM
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RC TISSUE-Retinal pigment epithelium;

RX MEDLINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E:A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Altechul J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhtting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Schautz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITINE-91352090; PubMed=1715583; Cybulsky M.I., Fries J.W.U., Williams A.J., Sultar Eyers M., Shows T., Gimbrone M.A. Jr., Collins T. "Gene structure, chromosomal location, and basis splicing of the human VCAM1 gene."; Proc. Natl. Acad. Sci. U.S.A. 88:7859-7863(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rajkumar N.R., Toth E.J., Submitted (AUG-2002) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Direct expression cloning of vascular cell adhesion molecule 1, cytokine-induced endothelial protein that binds to lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91016951; PubMed=1699207;
Polte T., Newman W., Gopal T.V.;
"Full length vascular cell adhesion molecule 1 (VCAM-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Umbilical vein;
                                                                                                                                    Jones E.Y., Harlos K., Bottomley M.J., Robinson R.C., Edwards R.M., Clements J.M., Dudgeon T.J., Stuart D.I. "Crystal structure of an integrin-binding fragment of adhesion molecule-1 at 1.8-A resolution.";
Nature 373:539-544(1995).
                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
MEDLINE=95147978; PubMed=7531291;
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Hession C., Tizard R., Vassallo C., Schiffer S.B., Goff D., Moy P.
Chi-Rosso G., Luhowskyj S., Lobb R., Osborn L.;
"Cloning of an alternate form of vascular cell adhesion molecule-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                        MEDLINE=95296382; PubMed=7539925;
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                                                                                        x-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
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J.-H., |
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Pepinsky R.B.,
Osborn L.;
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n C., Tizard R.,
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                            Liu J.-H.,
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PIR; A41288; A41288.

PIR; B41288; B41288.

PDB; 1VCA; 15-SEP-95.

PDB; 1VCA; 15-SEP-95.

PDB; 11J9; 07-NOV-01.

Genew; HGNC:12663; VCAM1.
                                        Pram; PF00047; ig; 6.

PRINTS; PR01472; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00408; IGc2; 3.

PROSITE; PS50835; IG_LIKE; 5.

Immunoglobulin domain; Glycoprotein; Cell adhesion; Repeat; Signal; Alternative splicing; Polymorphism; SIGNAL

1 24 PROBABLE
DOMAIN
TRANSMEM
                                                                                                                                                             InterPro; IPR003987; ICAM_VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; VCAM-1.
Pfam; PF00047; ig; 6.
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EMBL; M30257; AAA51917.1; ALT_TERM.
EMBL; M73255; AAA61270.1; -.
EMBL; M60335; AAA61269.1; -.
EMBL; AF536818; AAM96190.1; -.
EMBL; BC017276; AAH17276.1; -.
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-!- FUNCTION: IMPORTANT IN CELL-CELL ADHESION. INTERACTS WITH THE BETA-1 IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1 INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL TRANSDUCTION. THE VCAM1/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLE BOTH IN INMUNUME RESPONSES AND IN LEUKOCYTE EMIGRATION TO SITES OF INFLAMMATION.

-!- ALTERNATIVE PRODUCTS:

-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang J.-H.,
Osborn L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
Wang J.-H., Stehle T., Pepinsky R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular cell adhesion molecule 1 (VCAM-1): a cyclic peptide based the domain 1 C-D loop can inhibit VCAM-1-alpha 4 integrin interaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Sialoglycoprotein.

DISEASE: May play an important role in the genesis o artherosclerosis and rheumatoid arthritis.

SIMILARITY: Contains 7 immunoglobulin-like C2-type di DATABASE: NAME=PROW; NOTE=CD guide CD106 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd106.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
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ISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, as
il as on macrophage-like and dendritic cell types in both normal
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            VASCULAR CELL
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Liu J.-H., Karpusas
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                          WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS--NKALPAPIEK
                                                                                                                                                                                                                                                                                                                                  G--SFLTKGPSKLNDR------ADSRRSLWDQG-----NFP-----
                                                                                                                                                                                                                                                                                                                                                                                            LALLPAATQGNKV-----VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILG---NQ
TQIDS----PLSGKVRSEGTNST---
                                                                                      CPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
                                                                                                                   APEIFWSKKLDNGNLQHLSGNATLTLIAMRMEDSGIYVCEGVNLIGKNRKEVELIVQ---
                                                                                                                                                    SPSV---
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160.5; Ub ...
bred. No. 0.0062;
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
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                                                          PFTVEISPGPRIAAQIGDSVMLTCSVMGC--ESPSFSWR
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-LTLSPVSFENEHSYLCTVTCGHKKLEKGIQV
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CAM1_BRARE
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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NADL1.1
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10-OCT-2003
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                                                                                                         InterPro;
InterPro;
                                                                                                                                                       EMBL; X89204; CAA61490.1; -. PIR; T30581; T30581. HSSP; P20241; 1CFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cyprinidae; Danio.
                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Neurosci. Res. 42:547-561(1995)
              PRINTS;
                                                         InterPro; IPR003962;
InterPro; IPR007110;
InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     axonogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tongiorgi E., Bernhardt R.R., Schachner M
"Zebrafish neurons express two L1-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96155762; PubMed=8568941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                     gend
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SUBCELCULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in postmitotic neurones in 16-36 hour embryos, including those in the brain, cranial ganglia and
                                                                                                                                                                                                                                                                                                                                            initiation of axonogenesis in 16-36 hour embryos.
SIMILARITY: Belongs to the immunoglobulin superfamily.
Ll/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 5 fibronectin type III domains.
                                                      N; ZDB-GENE-980526-512; nadl1.1.
serPro; IPR008957; FN III-like.
serPro; IPR003961; FN III subd.
serPro; IPR003962; Fn III subd.
serPro; IPR007110; Ig-like.
serPro; IPR007598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: Onset
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              PF00047; 1g;
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                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WESNGQPENNYKT----TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
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(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
adhesion molecule Li.1 (N-CAM Li.1)
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Ostariophysi; Cypriniform
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Neurogenesis; Cell adhesion; Developmental protein; Glycoprotein;
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E; PS50835; IG_LIKE; 6.
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VDKSRWQQGNVFSCSVMHEALH-----NHYTQKSLSLS
                                                                                                                                            SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                                                                                                                                                             LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
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                                                                        IEGSLKVLDVQMEDM---GIYSCEVST-TLDSDTASGYITVQDKPDPPQSLKLSEKMER-
                                                                                              TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                      PQNLHVIRGSDAILHCK-----YTVDHNLKSPTVQ--WNKDG---HKITASTSNDKYHE
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                                                                                                                                                                                             T----LSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
                                                                                                                                                                                                                     THVHVVELPAQILTPDERLYQATAGQTVMLDCRTFGSPLPKIHWEILDSIPALSNAKISQ
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                                               TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD-----
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HUMAN
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"Structural rule of antibodies. Primary structure of a immunoglobulin-L-chain of the lambda type, subgroup IV protein Kern). V. The complete amino acid sequence and interpretation.";
Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE
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MEDLINE-70166723; PubMed-4909564;

Titani K., Wikler M., Shinoda T., Putnam F.W.;

"The amino acid sequence of a lambda type Benc complete amino acid sequence and the location
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IGLC1 AND IGLC2 AND IGLC3.
                                                               MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A
"Characterization of the two uniq
                                                                                                                                  "Amino acid sequence of the (lambda) immunoglobulin (IgG New)."; Biochemistry 13:1295-1302(1974).
                                                                                                                                                                        PARTIAL SEQUENCE (MYELOMA PROTEIN MEDLINE=74109253; PubMed=4814727; Chen B.L., Poljak R.J.;
                                                                                                                                                                                                                                                                                                           SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINE=71150336; PubMed=5549568;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE (BENCE-JONES PROTEIN NIG-64).
MEDLINE=83186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bence-Jones protein.";
Biochem. J. 110:631-652(1968).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 MEDLINE=75046825;
              X-RAY CRYSTALLOGRAPHY
                                                                                                          SEQUENCE (DOT).
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                                                                                                                                                                                                                                                                                                                                                   'Comparative studies on the structure of the light chains of immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
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PubMed=4215080;
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Genew; Genew;

HGNC:5855; IGLC1. HGNC:5856; IGLC2. HGNC:5857; IGLC3.

15-MAY-97 04-FEB-98

Genew; HGNC: MIM; 147220;

GO; GO:0003823; F:antigen binding; GO; GO:0006955; P:immune response; InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig\_MHC.

Pfam; PF00047; ig; 1. SMART; SM00407; IGc1; 1

PS50835; IG\_LIKE; 1.

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EMBL; J00253; AAA59107.1; AEMBL; L38562; AAB36581.1; AEMBL; X51754; CAB38569.1; AEMBL; X51755; CAA36049.1; AEMBL; X51755; CAA36051.1; AEMBL; X51755; CAA3605
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PDB; 2MCG; 15-JUL-92.
PDB; 7FAB; 31-JAN-94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=82080680; PubMed=6273747;
Hieter P.A., Hollis G.F., Kozemey
"Clustered arrangement of immunog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panagiotopoulos N.; "Rotational allomer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
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MISCELLANEOUS: Six tandem lambda-type genes were identified and the John the Mcg sequenced. These correspond to the Mcg sequenced (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz-
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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=75013804; PubMed=4415202;
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U.S.A. 71:3440-3444(1974).
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Abola E.E.,
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RESULT
SHS1_H
      RRRRRRROOCG CEEETT ACC
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Best Local S
Matches 31
localization of genes.";
Biochem. Biophys. Res. (2)
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                                                                                                                                                         Homo sapiens (Human, Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence
                                                                                                                                                                                                                                                                                                                                            SHS1_HUMAN
P78324; O00683;
Q9Y4U9;
                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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                                          Yamao T., Matozaki
Fujioka Y., Kasuga
"Mouse and human Sl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                        MEDLINE=97223399; PubMed=9070220;
                                                                                                        SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNNKYAASSYLSLTPEOWKSHRSYSCOVTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acozaki T., Amano K.,
Kasuga M.;
                                                                                                                                                                  (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
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                                                                                                                                                                                                                                                                                                                                                        STANDARD; PI
; 043799; Q8N517;
                                             SHPS-1: molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG MHC;
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100
104
5
                                                                                                                      (ISOFORM 1).
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                  Commun.
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Pred. No. 0.
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R -> K (IN OZ+ MARKER).
/FTId=VAR_003902.
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S -> G (IN KERN+ MARKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_003898
S -> T (IN MCG+ 1
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                                                                                                                                                               Catarrhini;
                                                                                                                                                                              Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTId=VAR
                  231:61-67 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCD9C7C201C13CC2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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QBTALB; (
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                                                                           Mateuda Y.,
                                             cloning of cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               003900
                                                                                                                                                                             Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          Q9H0Z2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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.00067;
                                                                                                                                                                                                                                                                                                                                                                         ξ
                                                                                                                                                               Hominidae;
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                                                                         Takahashi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
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                                                                                                                                                                                                                                                                                                                                                          Q9UDX2; Q9UIJ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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(Signal-
-2) (Sirp-alpha-
                                             chromosomal
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Gelfiths M.D., Gwilliam R., Hall R.E.,
RA Gratham D.V., Griffiths C., Griffiths M.D., Gwilliam R., Hall R.E.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howlen P.J.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howlen P.J.,
RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wilnes B.S., Wister P., Willey D.L., Williams L., Williams S.A.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RA Wiltehead S.L., Way P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Roders J.,
         TISSUE-Brain, Kidney, and Skin;
MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schu
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhai
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiel
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Sc
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pr.
                                                                                                                                                                       THR-52; ARG-54; ALA-57; GLY-7
GLY-109 AND VAL-131.
TISSUE=R-sin ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20053880; PubMed=10585853;
Sano S.-I., Ohnishi H., Kubota M.;
"Gene structure of mouse BIT/SHPS-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brooke G.P., Parsons K.R., Howard C.J.;
"Cloning of two members of the SIRP alpha family of protein t
phosphatase binding proteins in cattle that are expressed on
phosphatase binding proteins in cattle that are expressed on
and a subpopulation of dendritic cells and which mediate bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Monocytes;
MEDLINE=98143722; PubMed=9485180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (1 N-GLYCOSYLATION, AND TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
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4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAL-13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARG-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ullrich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kharitonenkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97215901; PubMed=9062191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A family
                                                                                                                                                                                                                                                              DNA sequence and comparative re 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALA-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۶.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of proteins that inhibit
 Loquellano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344:667-675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLY-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28:1-11 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND VAL-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORM 1),
Y-75; ASP-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM 1), PO ND INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM
                                                                                                                                                                                                      GLY-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sures
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                                                                                                                                                                                                      AND 2), A
ASP-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYMORPHISM, PHOSPHORYLATION, NS WITH PTPN11; PTPN6 AND GRB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND VARIANTS LEU-44; THR-50; THR-52; LEU-96; ASN-100; ARG-107; GLY-109 AN
                                                                                                                                                                                                                                                                                analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                  L.H., Derge J.G.,
Shenmen C.M., Schuler G.D.
Thaefer C.F., Bhat N.K.,
Thaefer T., Heleh F.,
                                                                                                                                                                                                      AND VARIANTS LEU-44; THR-50; LEU-96; ASN-100; ARG-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASP-95;
                                                                                                                                                                                                                                                                                  human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mediate binding
                                                                                                                                                                                                                                                                                  chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEU-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine
                 Scheetz T.E., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲,
Mullahy
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1 monocytes
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk syllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Latour S., Tanaka H., Demeure C., Mateo V., Rubio M.,
Maliszewski C., Lindberg F.P., Oldenborg A., Ullrich /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multi-protein complexes in macrophages.";
Curr. Biol. 9:927-930(1999).
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Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd.
Schraven B., Neel B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells. SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro. Binds FGR (By similarity). Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B. SUBCELIULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 167:2547-2554 (2001).

Immunol. 167:2547-2554 (2001).

FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PrDN6, PTPN11 and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function (By similarity). Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin. Mediates negative regulation and service of the coupled cellular responses induced by cell achieves the coupled cellular responses induced by cellular responses ind
                          pancreas.
PTM: N-gl
                                                                                                                                     Note=No experimental conf
TISSUE SPECIFICITY: Ubiquit
Detected on myeloid cells,
                                                                                                                                                                                                                                                         Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
                                                                                                           levels in heart,
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vote=No experimental confirmation av
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                                                                                 placenta, prostate,
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                                                                           tal confirmation available;

Ubiquitous. Highly expressed in brain.

Ubiquitous Totalis. Detected at lower

acenta, lung, testis, ovary, colon, liver,

ostate, spleen, kidney, skeletal muscle an
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tyrosine residues
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21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last ann
Ig lambda chain C region.
Sus scrofa (Pig).
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P01846;
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                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stimulation with EGF, growth hormone, insulin and PDGF.
Dephosphorylated by PTPN11.
-!- SIMILARITY: Contains 1 immunoglobulin-like C1-type domain:
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                       NCBI_TaxID=9823;
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PIR; JC5287; JC
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or send an email to license@isb-sib.ch).
MEDLINE=78000254; PubMed=409425
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AL049634; CAB46662.1; ALT SEQ.
AL117335; CAC12723.1; -.
BC023692; AAH26692.1; -.
BC033092; AAH33092.1; -.
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AC004832; AAF19260.1;
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5; Mismatches 15
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MEDLINE-88196070; PubMed-3129289;
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                                               InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00047; 1g; 1.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                       EMBL; M35582;
HSSP; P01842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mami F., Cazenave P.A., Kindt T.J.; "Conservation of the immunoglobulin C lambda 5 gene in the EMBO J. 7:117-122(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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10-OCT-2003
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01-FEB-1991 (Rel. 17, Created)
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nterPro; IPR003006; Ig_MHC.
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SIMILARITY: Contains 1 immunoglobulin-like domain
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M00407; IGC1; 1.
PS50835; IG_LIKE; 1.
PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835; IG_LIKE; 1. PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AA;
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104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 17, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                             AAA39152.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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35.2%;
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Pred. No. 0.001;
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; 3817AAEBD747C396 CRC64;
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RESULT 83
KACB_RABIT
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Best Local S
Matches 32
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Best Local (
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DISULFID
SEQUENCE
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin
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NON TER 1 1

DOMĀIN 6 100 IG-LIKE.

DISULFID 27 86

DISULFID 104 104 INTERCHAIN (WITH H

SEQUENCE 105 AA; 11674 MW; AAB417DF68471A17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin lambda-chains.
Biochem. J. 197:177-183(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-FEB-1991 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82091105; PubMed=6797414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specificity.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
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    -!- MISCELLANEOUS: This lambda chain expresses the c7 allotypic

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                                                                                                                                                      FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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                                                                                                       AASSFLHLTANQWKSYQSVTCQVTHE---GHTVEKSLA 100
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32.7%;
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Pred. No. 0.00
17; Mismatches
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B427513272E8663D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE
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AAB417DF68471A17 CRC64;
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Matches 31
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P06731;
01-JAN-1988
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21-JUL-1986
15-MAR-2004
                                                                                                                                                                                             HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multiplicity of constant kappa light chain genome: a b4b4 homozygous rabbit contains a EMBO J. 2:437-441(1983).
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PROSITE; PS00290; IG_MHC; FALSE_NEG.
Immunoglobulin domain; Immunoglobulin
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InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGcl; 1.
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  OR CEA
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utheria; Lagomorpha; Leporidae; Oryctolagus.
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EV the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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Zimmermann W., Ortlieb B., Friedrich R., von Kl
"Isolation and characterization of cDNA clones
carcinoembryonic antigen reveal a highly conser
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Oikawa S., Nakazato H., Kogaki G.;
"Primary structure of human carcinoembryonic antigen
from cDNA sequence.";
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Barnett T., Goebel S.., Nothdurft M.A., Elting J.J.
"Carcinoembryonic antigen family: characterization
for NCA and CEA and suggestion of nonrandom sequenc
their conserved loop-domains.";
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SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 7 immunoglobulin-like domains. DATABASE: NAME-PROW; NOTE-CD guide CD66e entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd66e.htm".
   M17303;
M59256;
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EMBL; M15042; AAA51963.1; -
EMBL; M16234; AAA51972.1; -
PIR; A36319; A36319
PDB; 1E07; 04-JUL-00.
Genew; HGNC:1817; CEACAM5.
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SIGNAL
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PROSITE; PS50835; IG_LIKE; 6.
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DSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                                                         QELFIPNITVNNSGSYTCQAH-------NSDTGLNRTTVTTITVYAEPPKPF
                                                                                                                                                                                                          RSGENLNLSCHAASNPPAQYSWFVN
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                                                                                                                                                                FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP----
                                       ITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRN 386
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                                                                                                                                                                                                                                                                                          Score 151.5;
Pred. No. 0.02
78; Mismatches
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IG-LIKE 3.
IG-LIKE 4.
IG-LIKE 5.
IG-LIKE 6.
IG-LIKE 7.
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                                               Query Match
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Matches 29
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DISULFID
SEQUENCE
                                                                                                                                      Immunoglobulin
NON TER 1
DOMAIN 5
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21-JUL-1986
21-JUL-1986
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Allelic forms of rat kappa chain genes: evidence "Allelic forms of rat kappa chain genes: evidence and the level of nucleotide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                           Pfam; PF00047; ig; 1. T
SMART; SM00407; IGC1; I. 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DA;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   PIR; A02118; K1RTA.
HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82082587; PubMed=6273908;
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21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig kappa chain C region, A allele.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                             Similarity
             PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS-----
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PTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRD-----GVLDSVTDQD
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                                                                                                   106 AA;
                                                                                                                                                                 domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                          5.6%;
                                                                                                   11732 MW;
                                               Score 150; DB
Pred. No. 0.00
23; Mismatches
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on update)
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nes 28;
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                                                                                                                 HEAVY CHAIN)
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Matches 56
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Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC: II beta;
SWART; SW00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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PIG
HB2C_PIG
P15982;
01-APR-1990
                                                                                                                          TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sache D.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor.
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ haplotype C beta chain
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15-JUL-1999
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000353; MHC_II_beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of
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expression of two allelic class II
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            240
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                                                                                                                                                                                                                                                       Transmembrane;
                                                                                          Similarity
          RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                GLWTAAL-----TVMLVVLGAPVAEGRD-----SPQDFVFQFK-GECYFYN
                                                       GTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMIS
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guern C., Hirsch
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205
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Cetartiodactyla; Suina;
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                                                                                          5.5%;
23.2%;
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                                                                              Pred. No. 0.0
); Mismatches
                                                                                          Score 149.5;
Pred. No. 0.
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BY SIMILARITY.
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                                                                                                                           AA9581F2A3B1969D CRC64;
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(See http://www.isb-sib.
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ina; Suidae;
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Sus.
                                                                                                                                      (POTENTIAL)
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Q9Z0<del>J</del>8;
30-MAY-2000
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SIGNAL
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                                                                                                                                                                                                                                                                                    use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-I-TISSUE SPECIFICITY: Highly expressed in brain.
-i- PTM: Glycosylated.
-i- SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Funatsu N., Miyata S., Kumanogoh H., Shige
Sokawa Y., Maekawa S.;
"Characterization of a novel rat brain gly
anchored protein (Kilon), a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 CARBOHYD
                                                                                                                                                                                                  Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                   EMBL; AB017139; BAA75649.1;
                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: CELL-ADHESION (POTENTIAL).
-1- SUBCELLULAR LOCATION: Attached to the membrane
-1- TISSUE SPECIFICITY: Highly expressed in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=99175207; PubMed=10075727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
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                                                                                                                                                                                        PROSITE;
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InterPro; IPR003598; Ig_c2.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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POTENTIAL.
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Sciurognathi; Muridae;
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the IgLON cell adhesion molecule
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CARBOHYD
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P01834;
                                                                                Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa type, subgroup 3 (Bence-Jones prote Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
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21-JUL-1986 (Rel. 01,
15-MAR-2004 (Rel. 43,
                    SEQUENCE FROM N.A.
MEDLINE=81042304;
                                                                                                                                                                                                                                                                                   Biochemistry
                                                                                                                                                                                                                                                                                                  Gall W.E., Edelman G.M.;
"The covalent structure of a human Intrachain disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=71064023; PubMed=5489770;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                MEDLINE=72188439; PubMed=5027703;
                                                                                                                                                                                                                                      SEQUENCE
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  Max E.E.,
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                        PubMed=6775818,
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Pred. No. 0.013;
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  J.G.,
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-LINKED (GLCNAC. . .)
37E90D1C7D24ACAB CRC6
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man gamma G-immunoglobulin. VI.
                                                                                                                                                                                                                                                                                                                         gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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    Maizel J.V. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                         G-immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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    Leder
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the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gamma
New Yo
                 Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
                                                                                          XIX;
                                                                                                                                                                                              EMBL; J00241; AAA58989.1; EMBL; V00557; CAA23823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (BENCE JONES PROTEIN ROY).
Hilschmann N., Barnikol H.U., Hees M.,
Steinmetz Kayne M., Suter L., Watanabe
(In) Franck F., Shugar D. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes conserve homology
Cell 22:197-207(1980).
                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98249779; PubMed=9588180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=70201507; PubMed=5447531; Kohler H., Shimizu A., Paul C., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The amino acid sequence of a kappa type Bence-Jones complete sequence and the location of the disulfide by Biol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=69234734; PubMed=4893682; Titani K., Shinoda T., Putnam F.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (BENCE-JONES PROTEIN CUM MEDLINE=68242259; PubMed=5586923;
                                                                                                  Genew;
                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Abdominal adipose
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Macroglobulin structure:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoppe-Seyler's Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloned human and mouse
                                                                    GO:0003823; F:antigen GO:0006955; P:immune r
                                                                                                             1172;
1MIM;
                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics
                                                                                                                                 1D6V; 04-OCT-00.
1HEZ; 18-JUL-03.
1HKL; 12-MAR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete amino acid
                                                                                                                                                               1D5B; 09-FEB-00.
1D5I; 09-FEB-00.
                                                                                                                                                                                     B90562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       globulins: structure and function,
                                                                                                   HGNC:5716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WALDENSTROM'S MACROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BENCE-JONES
                                                                                                             08-AUG-01.
15-MAY-97.
                                                                                                                                                                                     кани.
                                                                                                   IGKC
                                                                                                                                                                                                                                                                                                                                                                                                                     38-41 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kappa immunoglobulin constant
in functional segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of
                                                                            binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable
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                                                                                                                                                                                                                                     agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                     62-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putnam
                                                                                                                                                                                                                                                 removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bence Jones protein
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S.;
                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pp.57-74,
                                                                                                                                                                                                                                      http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В.,
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bridges.";
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PS50835;

IG\_LIKE; 1

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RESULT 89
NFAS_CHICK
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                            NFAS CHICK S: 042414; Q90924; 15-MAR-2004 (Rel 15-MAR-2004 (Rel 15-MAR-2004 (Rel 15-MAR-2004 (Rel
                                                                                              "Organization of the neurofascin gene and analysis of developments regulated alternative splicing.";
J. Biol. (Chem. 272:28742-2879(1997).
-i- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis myelination and neuron-glial cell interactions (By similarity)
-i- SUBCELTULAR LOCATION: Type I membrane protein.
-i- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                 MEDLINE=92317154; PubMed=1377696; Volkmer H., Hassel B., Wolff J.M., Franker B., Wolff or ereconstructure of the axonal surface reconstructure of the axonal subgroup confermity "
                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID
                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                 superfamily.";
J. Cell Biol. 118:149-161(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                          MEDLINE=98019255; PubMed=9353344;
                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                        Neurofascin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin
                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
DEVELOPMENTAL STAGE: There is one major 'early' isoform ar multiple 'late' isoforms. Around 50 isoforms are found at different developmental stages.

PTM: N-glycosylated and O-glycosylated.

PTM: May be proteolytically cleaved at Arg-636.

SIMILARITY: Belongs to the immunoglobulin amonfolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG--QPENNYKTTPPVLDSDGS
                                                                                IsoId=042414-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ഗ
                                                                                                                                                                                                                                                                                                                  AND 801-815,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 43,
(Rel. 43,
(Rel. 43,
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106
83
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                  (ISOFORM 2),
5, CLEAVAGE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
86
106
83
                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Weognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11609
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57
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29.5%;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V -> L (IN INV(1,2) MARKER)

/FIId=VAR 003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

M; 51984D1FDD372CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 148; DB 1; Length 106; Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH A HEAVY CHAIN).
V -> L (IN INV(1,2) MARKER).
                                                                                                                                                                                                                                                                                                                   ΑT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                   recognition of the
                                                                                                                                                                                                                                                                                                                 ARG-636, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region; 3D-structure.
                                                                                                                                                                                                                                                                                                                            얶
                                                                                                                                                                                                                                                                                                                             26-46;
                                                                                                                                                                                                                                                                   Rathjen F.G.; molecule neurofascin immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                   GLYCOSYLATION
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                                                                                                                                                                                                                                                                                                                             637-641;
                                                    isoform and
                                                                                                                                                  synaptogenesis
                                                                                                                                                                                        developmentally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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      Pfam; PF00041; fn3; 5.

Pfam; PF00047; ig; 6.

SMART; SM00060; FN3; 5.

SMART; SM00408; IGC2; 3.

PROSITE; PS50835; IG LIKE; 6

Cell adhesion; Repeat; Signa
               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                      DISULFID
DISULFID
DISULFID
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DOMAIN
TRANSMEM
                                                                                         DISULFID
DISULFID
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DOMAIN
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EMBL;
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SIGNAL
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InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003961;
InterPro; IPR008957;
                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X65224; CAA46330.1;

X14341; CAA74726.1;

X14342; CAA74726.1;

X14343; CAA74726.1;

X14343; CAA74726.1;

X14344; CAA74726.1;

X14346; CAA74726.1;

X14347; CAA74726.1;

X14348; CAA74726.1;

X14349; CAA74726.1;

X14349; CAA74726.1;

X14349; CAA74726.1;

X14349; CAA74726.1;

X14349; CAA74726.1;

X14350; CAA74726.1;

X14350; CAA74726.1;

X14350; CAA74726.1;

X14350; CAA74726.1;

X14350; CAA74726.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  S26180; S26180.
; P20241; 1CFB.
                                                                                                                                                           840
943
1134
1052
     636
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262
355
448
539
643
742
                                                                                                                                                                                                                                                                                                                           Alternative
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1052
1207
1207
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1235
1369
1369
231
231
231
7350
                                                                                                                                                                                                                                                                                                                                                                                           FN_III.
; FN_III-like.
; Ig-like.
; Ig_c2.
                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
                                                                                                                                                                                                                                                                                                                           splicing
                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 111 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
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SIMILARITY: Contains 5 fibronectin type III domains.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
                                                                                                                                                                                     moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Transmembrane; Immunoglobulin domain;

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LAMP HUMAN

ILAMP HUMAN

ID

AC

Q13449;

DT

O1-NOV-1997 (Rel. 35, Created)

DT

O1-NOV-1997 (Rel. 35, Last sequence upday

DT

O1-NOV-1997 (Rel. 36, Last sequence upday

DT

O1-NOV-1997 (Rel. 37, Last sequence upday

DT

O1-NOV-1997 (Rel. 37, Created)

CC

Membria System-associated membrane protein

ON

CMAMMalia; Eutheria; Primates; Catarrhini

ON

Membria Subteria; Primates; Catarrhini

ON

NCBI_TaxID=9606;

RN

(1)

RN

SEQUENCE FROM N.A.

MEDLINE=96235133; PubMed=8666243;

RP MEDLINE=96235133; PubMed=8666243;

RP MEDLINE=96235133; PubMed=8666243;

RP MEDLINE=96235133; PubMed=8666243;

RR

GENRAL Cloning and structural analysis of

RT

Gene 170.189-195(1996).

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CONTRIBUTES TO THE GUIDANCE OF DEVELO
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Missing (in isoform 2).
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Pred. No.
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Catarrhini; Hominidae
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Matches 75
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SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell &
Repeat; Signal; Lipoprotein.
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                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROW OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tract
as well as in single layers of the superior colliculus, spinal
chord and cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chord and cerebellum. SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON \,
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75; Conser
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SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA---KTKPREEQ
                                                                   SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEY
                                                                                                                                       LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
                                                                                                                                                              LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF
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                     LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPP-TITESKSNEAT
                                           LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
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Pred. No. 0.01
19; Mismatches
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IG-LIKE C2-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration - MBL outstation -
                                                                                                                                                                                                            78;
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                                                                                                                                                                                                           Gaps
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"Expression patterns of L1-family cell recognition molecules L1, CHL1,

"I recam, and neurofascin in the mouse brain.";

I NrCAM, and neurofascin in the mouse brain.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis,

C myelination and neuron-gilal cell interactions (By similarity).

C -!- SUBUNIT: Probable constituent of a neurofascin/NRCAM/ankyrin G complex. Associates with the sodium channel beta-1 (SCN1B) and beta-3 (SCN1B) subunits (By similarity).

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                          Pfam; PF00041; fn3; 4.
Pfam; PF00041; fg; 6.
SMART; SM00060; FN3; 4.
SMART; SM00409; IG; 6.
SMART; SM00408; IGc2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JLT 91

S_MOUSE

NFAS MOUSE

Q810Ü3;

15-MAR-2004

15-MAR-2004

15-MAR-2004
                                                                                                Glycoprotein.
SIGNAL
CHAIN 2
              TRANSMEM
DOMAIN
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or send a
                                                                                                                                                                                                                                                                                              EMBL;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                    DOMAIN
                                                                                                                                    Cell adhesion; Repeat; Signal;
                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                 MGD; MGI:2442229; D430023G06Rik.
                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Swiss Webster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFASC
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                                                                                                                                                                                                                                                          InterPro; IPR003961; FN_III.
InterPro; IPR008957; FN_III-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                    is SWISS-PROT entry is copyright. It is produced through a collaboration tween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its e Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way dified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 6 immunoglobulin-like C2-type d SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                                                                                                                                                                                               AJ543322; CAD65849.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor.
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230
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Last
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                                                                                                                                                                                                                                                          _III-like.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
                                                                                    NEUROFASCIN.
EXTRACELLULAR
                                                                                                             POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                   Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1240
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                                                                                    (POTENTIAL).
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RESULT 92
NPHN_MOUSE
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Best Local
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
NCBI_TaxID=10090;
[1]
                                                                              Q9QZS7;
28-FEB-2003
28-FEB-2003
10-OCT-2003
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                                                        Nephrin precursor NPHS1 OR NPHN.
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                                                                                                                                                                                EP---LQSAPPNPNREVAGDTIIFRDTQISSRA-----VYQCNTSNE
                                                                                                                                                                                                           QPENNYKTTPPVLDSD-
                                                                                                                                                                                                                                                         APIEKTIS-KAKGQP----REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                    IDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPE--VTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                           PVIFWMSSSMEPITQDKRVSQGHNGDLYFSNVMLQDMQTDYSCNARFHFTHTIQQKNPFT
                                                                                                                                                                                                                                                                                                                                                                                        PSVQCRSPRGKNIQGGKTLS-----VSQLELQDSGT-WTCTVLQN-----
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                                                                                                                                                                                                                                   GSIRHTISVRVKAAPYWLDEPKNLILAPGEDG
                                                                                                                                                                                                                                                                                                      DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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                                                                                                                                                                                                                                                                                 - PTPDIAWYKKGGDLPSNKAK--FENFNKALRITNVSEE-----DSGEYFCLASNKM--
                                                                 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
rursor (Renal glomerulus-specific
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                                           (Mouse)
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                                Chordata;
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Pred. No. 0
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                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                              -PS-FMYPQGTSSSQMVLRGMDLLLECIASGV---
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(GLCNAC...
(GLCNAC...
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                                                                   cell
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                                                                   adhesion receptor)
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MGD; MGI:1859637; Nphal.

GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007254; P:JNK cascade; IDA.
GO; GO:000165; P:MAPKKK cascade; IDA.
InterPro; IPR009957; FN III-like.
InterPro; IPR009957; FN III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn; 1.
Pfam; PF00041; fn; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; PS0035; IGC3; 1.
SMART; PS0035; IGC3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
 Immunoglobulin SIGNAL 1
CHAIN 23
DOMAIN 1065
DOMAIN 1085
DOMAIN 25
DOMAIN 135
DOMAIN 340
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DOMAIN 740
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DOMAIN 740
DOMAIN 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diaphragm,
J. Clin. In
-!- FUNCTIC
                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There use by non-profit institutions as long smodified and this statement is not removed. I entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH CD2AP.

MEDLINE=21590051; PubMed=11733379;

Shih N.Y., Li J., Cotran R., Mundel P.,

"CD2AP localizes to the slit diaphragm;

novel C-terminal domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Podocin, a raft-associated component of the g diaphragm, interacts with CD2AP and nephrin.", J. Clin. Invest. 108:1621-1629(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwarz K., Simons M., Reiser J., S
Shaw A.S., Holzman L.B., Mundel P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH CD2AP AND NPHS2. MEDLINE=21590460; PubMed=11733557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>≅</u>∄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nephrin localizes cell.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney Int.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holzman L.B., St
Abrahamson D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99436348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein (Potential at podocyte slit diaphragm between podocyte foot process ITSSUB SPECIFICITY: Expressed in kidney glomeruli.

PTM: Phosphorylated on tyrosine residues (By similarity)
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 8 immunoglobulin-like domains.
SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Seems to play a role in the development or the kidney glomerular filtration barrier. May anchor slit diaphragm to the actin cytoskeleton. SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Pathol. 159:2303-2308(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SMISS-PROT entry is copyright. It is produced through a collaboration and the EMBL outstreen the Swiss Institute of Bioinformatics and the EMBL outstreen the Swiss Institute of Bioinformatics are no restrictions as long as its content is in and for con
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                                                                                                                                                                                     domain;
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G-LIKE C2-TYPE 1
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RESULT 93
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AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence upda
DT 10-OCT-2003 (Rel. 42, Last annotation up
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota, Metezoa; Chordata; Craniata;
OC Mammalia; Eutheria; Rodentia; Sciurognat
OX NCBI_TaxID=10116;
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; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat

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RESULT 94
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Matches 34
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS508390; IG_MHC; 1.
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                                                                                                                                                                                                                                            Q05695;
Q01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule L1 precursor (N
                                                                            Miura M., Kobayashi M., Asou H., Uyemura K.; "Molecular cloning of cDNA encoding the rat neural cell adhesion molecule L1. Two L1 isoforms in the cytoplasmic region are produc by differential splicing "; FEBS Lett. 289:91.95(1991).
                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentiation of the statement are not removed. Usage by and for contentiation of the statement are not removed.
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                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE=91372414; PubMed=1894011;
                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                CAME
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HSSP; P01842; 7FAB
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or send an email to license@isb-sib.ch).
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MEDLINE=87305594; PubMed=3114047;
adhesion, neurite fasciculation, outgr
to axonin on neurons.
SUBCELLULAR LOCATION: Type I membrane
ALTERNATIVE PRODUCTS:
                                                     FUNCTION: Cell adhesion molecule with development of the nervous system. Inv
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Sciurognathi; Muridae; Murinae; Rattus.
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InterPro; IPR003961; FN_III.

InterPro; IPR007110; Ig-1ke.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 4.
Pfam; PF00047; ig; 6.
SMART; SM00060; FN3; 4.
SMART; SM00408; IGc2; 5.
SMART; SM00408; IGc2; 5.
PROSITE; PS50815; IG LIKE; 6.
Neurogenesis; Cell adhesion; Developmental protein; G1.
Transmembrane; Repeat; Immunoglobulin domain; Signal;
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IsoId=Q05695-2; Sequence=VSP 002592;
IsoId=Q05695-2; Sequence=VSP 002592;
-!- TISSUE SPECIFICITY: Isoform 2 is predominantly found in the peripheral nervous systwhile isoform 1 is found in the peripheral nervous systwhile isoform 1 is found in the peripheral nervous system.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X59149; CAA4180
PIR; S36126; S36126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            CARBOHYD
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FN_III.
Ig-like.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 111 1
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NEURAL CELL ADHESION MOLECULE
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most proposed in the statement as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
119-OCT-2003 (Rel. 42, Last annotation update)
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EMBL; X04768; CAA28461.1; -. PIR; B26167; B26167. HSSP; P01842; 7FAB.
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Best Local
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InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                  Immunoglobulin
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DISULFID
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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DISULFID
VARIANT
                                                                                                                                                                                 "The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes.";
J. Immunol. 115:59-62(1975).
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                      Sheppard H.W., Gutman G.A.;
"Allelic forms of rat kappa chain genes: evidence selection at the level of nucleotide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                                                                                                                                                            Starace V., Querinjean
                                                                                                                                                                                                                                                                                                                             STRAIN=Louvain;
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig kappa chain C region, B allele.
Rattus norvegicus (Rat).
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SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                       PIR; A93901; K1RTB.
                                                                                                                                                                                                                                       MEDLINE=75212238; PubMed=807630;
                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN S211).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Bayer B.A., Helt G., Welson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dolchan J.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 29
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CONFLICT
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01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Berkeley:
Calniker S.E., Pfeiffer B.D., Knafels J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Oregon-R;
MEDLINE=89028670; PubMed=3141062;
Seeger M.A., Haffley L., Kaufman T.C.;
"Characterization of amalgam: a member of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker S.E.,
Palazzolo M.J.;
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Eukaryota; Metazoa; Arthropoda; Hrzapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amalgam protein precursor.

AMA OR BG:DS00276.6 OR CG2198.
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O., RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;

"The genome segmence of Prozophila melasocarter"
               Query Match
Best Local
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=Berkeley; TISSUE=Embryo;

MEDLINE=22426066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Char

George R.A., Guarin H., Kronmiller B., Pacleb J.M.,

Rubin G.M., Celniker S.E.;

"A Drosophila full-length cDNA resource.";

"A Drosophila full-length cDNA resource.";
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GO; GO:0005886; C:plasma membrane;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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EMBL; AY051911; AAK
PIR; A31923; A31923
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EMBL; AE001572; AAD19797.1
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SMART; SM00408; IGc2; 2
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                                                                          CONFLICT
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Liu X., Mattei B., McIntosh T.C., McLeod N
                                                                                                                                                                                                                                                                                                 PROSITE;
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               Similarity
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; AAK93335.1; -.
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333
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57; Mismatches
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01-APR-1993
10-OCT-2003
                                                                                                                                                                         Cybulsky M.I., Allan-Motameu H., CULL-
"Structure of the murine VCAM1 gene.";
Genomics 18:387-391(1993).
                                                                                                                                                                                             STRAIN=129; TISSUK=EMULIV.,
MEDLINE=94117008; PubMed=7507076;
Cubulsky M.I., Allan-Motamed M., Collins
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P29533;
STRAIN=FVB; TISSUE=Lung;
MEDLINE=93232042; PubMedd-7682556;
MOY P., Lobb R., Tizard R., Olson D.,
"Cloning of an inflammation-specific p
form of murine vascular cell adhesion
J. Biol. Chem. 268:8835-8841(1993).
                                                                                                                                                                                                                                                              Araki M., Araki K., Vase "Cloning and sequencing Gene 126:261-264(1993).
                                                                                                                   STRAIN=NIH Swiss, and Kumar A.G., Dai Y.X., Ballantyne C.M.,
                                                                                                                                                                                                                                                                                                              TISSUE=Lymph node
MEDLINE=93246254;
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MEDLINE=92181437;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular cell adhesion protein 1 precursor (V-CAM VCAM1 OR VCAM-1.
                                                                              SEQUENCE FROM N.A.
                                                                                                       Submitted (AUG-1994) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                               92181437; PubMed=1371918;
C., Moy P., Tizard R., Chisholm P., Willia
Niyake K., Kincade P., Lobb R.;
of murine and rat vascular cell adhesion
Biophys. Res. Commun. 183:163-169(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
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(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
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Kozak C
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modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korenaga R., Ando J., Tsuboi H., Kamiya A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION
IN LEUKOCYTE-ENDOTHELIAL CELL ADHESTON. INTERACTS WITH THE BETA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95015899; PubMed=7523515;
Kumar A.G., Dai X.Y., Kozak C.A.,
Ballantyne C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [6]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Terry R.W., Kwee L., Levine J.F., Labow "Cytokine induction of an alternatively adhesion molecule (VCAM) mRNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Endothelial cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93317595; PubMed=7687058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Murine VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and inflamed tissue.

PTM: The GPI-anchor is located on position 319 of isoform 2 SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P29533-2; Sequence=VSP_002581, VSP_002582; TISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, well as on macrophage-like and dendritic cell types in both nor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND STRANSDUCTION. THE VCAM1/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES AND IN LEUKOCY EMIGRATION TO SITES OF INFLAMMATION. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG ISOFORM) ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (SHORT ISOFORM). ALTERNATIVE PRODUCTS:

BY AND ALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=Short
IsoId=P29533-2; Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Long;
IsoId=P29533-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular cloning,
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L outstation -
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EMBL; U12879; U12880; U12874; U12871; U12883; U12881; U12881; U12882; U128875; L22349; U12878; L22355; L22301; M84487; AAA16921.1; AAA16921.1; AAA16921.1; AAB60661 AAB60662 AAA16920 AAA16920 CAA47989.1; AAA16921 AAA16921.1; AAA16921.1; AAA16921.1; AAA16921.1; AAA40545.1; AAB60659 AAA16920 JOINED.
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Best Local
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GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR00398; Ig-cl.
InterPro; IPR003598; Ig-cl.
InterPro; IPR003598; VCAM-1.
PERNTS; PF0047; ig; 5.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
PRINTS; PR01476; ICCAM1.
SMART; SM00408; IGC; 3.
PROSITE; PS50835; IG_LIKE; 5.
Immunoglobulin domain; Glycoprotein; Cell adhesion; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U12872; 
EMBL; U12873; 
EMBL; U12873; 
EMBL; U12877; 
EMBL; L12877; 
EMBL; L08431; 
EMBL; L12541; 
EMBL; U42327; 
EMBL; U42327; 
                                                                                                                                                                                                      CONFLICT
SEQUENCE
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CARBOHYD
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DISULFID
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DOMAIN
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SIGNAL 1
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JN0581; JN0581.
                                                                                271
                                                                                                                        237
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                                                                                                                                            32
                                                                                                                                                                         Similarity
 TLEKRTQV-
                   KVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP----KDTLMISRTPEVTCV
                                       VVLTCAAIGCDSPSFSWRTQTDSPLNGVVRNEGAKSTLVLSSVGFEDEHSYLCAVTCLQR
                                                          LTLTLESPPGSSPSVQCRSPRGKNIQG------GKTLSVSQLELQDSGTWTCTVLQNQK
                                                                               SGNATLTLIAMRMEDSGVYVCEGVNLIGRDKAEVELVVQEKPFIVDISPGSQVAAQVGDS
                                                                                           QGNFPLIIKNLKIEDSDTYICE----VEDQKEEVQLLV------FGLTANSDTHLLQGQS
                                                                                                                       QEGGAVTMTCSSEGLPAPE1FWGRKLDNEVLQLL-----
                                                                                                                                           KKGDTVELTCTASQKKSIQFHW--KNSNQI-KILGNQGSFLTKGPSKLNDRADSRRSLWD
                                                                                                                                                                                                   693
739
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                                                                                                                                                                Conservative
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AAA80014.1;
AAA80015.1;
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AAA40546.1;
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81317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal;
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ALT_SEQ.
ALT_SEQ.
ALT_SEQ.
                                                                                                                                                                                                       XW.
                                                                                                                                                             78;
                                                                                                                                                                                                     /FTId=VSP_002581.
Missing (In isoform 2
/FTId=VSP_002582.
/FTId=VSP_002582.
D -> N (IN REF. 3).
D -> N 3D2134C341E5E449 CR
                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing.
                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                              BY SIMILA
                                                                                                                                                                         Score 144.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
EKPFTVDISPGSQVAAQVGDSVVLTCAAIGCDSPSF ->
GRMKSQITNGHQLTVHLMFAKSFYFICYLCLYLAL (in
                                                                                                                                                                                                                                                                                                          N-LINKED
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D (GLCNAC. .
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                                                                                                                                                                                                      CRC64;
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(POTENTIAL).
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RESULT 99
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Pfam; PF00047; ig; 3. SMART; SM00408; IGc2; 2. SMART; SM00408; IGc2; 2. SMSTE; PS50835; IG LIKE; 3. Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein. 28
                                                                                                EMBL; U31554; AAA86120.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2.
                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAMP_RAT
Q62813;
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol.NOV-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Limbic system-associated membrane protein pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSAMP OR LAMP
                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING. CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELLING OF MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTHE HYPOTAMPAL MOSSY FIBER PROJECTION.

SUBGELLULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic associated cortical and subcortical regions that function in cognition, memory, and learning. AT STAGE E20 IT IS DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16 AREAS OF THE THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC THALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                        family
                                                                                                                                                                                                                                                                                                                                                                          REGION
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Sciurognathi; Muridae;
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Tait S., Collinson J.
Submitted (NOV-2001)
TISSUE=Brain;
MEDLINE=97103184; PubMed=8947556;
MEDLINE=97103184; PubMed=8947556;
                                                                                                                                              P97685; P97684; Q91Z60;
15-MAR-2004 (Rel. 43, Czeated)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                    NFAS_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                  TISSUE-Brain
                            SEQUENCE OF 25-1240
                                                                         SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=10116;
                                                                                                                   Rattus norvegicus (Rat).
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Pred. No. 0
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                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0B76AFDD68A39BB6 CRC64;
                                                      P.J.;
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Ratcliffe C.F., Westenbroek R.E., Curtis R., Catterall W.A.;
"Sodium channel betal and beta3 subunits associate with neurofascin
through their extracellular immunoglobulin-like domain.";
J. Cell Biol. 154:427-434 (2001).

-!- FUNCTION: Cell adhesion, ankyrin-binding protein which may be
involved in neurite extension, axonal guidance, synaptogenesis,
myelination and neuron-glial cell interactions. Isoforms 2/3 may
be responsible for mediating and signaling axon-glial interaction
                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=NF186, 186 kDa isoform;
IsoId=P97685-1; Sequence=Displayed;
Name=2; Synonyms=NF155, 155 kDa isoform;
IsoId=P97685-2; Sequence=VSP_050416, VSP_050417, VSP_050418,
VSP_050419;
Name=3; Synonyms=NF155, 155 kDa isoform;
IsoId=P97685-3; Sequence=VSP_050416, VSP_050417, VSP_08411,
VSP_050418, VSP_050419;
-!- TISSUE SPECIFICITY: Isoform 1 is expressed at Nodes of Ranvier while isoform 2/3 is expressed in unmyelinated axons.
-!- DEVELOPMENTAL STAGE: Strongly but transiently up-regulated in oligodendrocytes at the onset of myelinogenesis. Once these last have engaged their target exons, expression declines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tait S., Gunn-Moore F., Collinson J.M., Huang Pedraza L., Sherman D.L., Colman D.R., Brophy "An oligodendrocyte cell adhesion molecule at the paranodal axo-glial junction.";
J. Cell Biol. 150:657-666(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION OF ISOFORMS 1 AND 2/3, INDIRECT PHOSPHORYLATION, AND TISSUE SPECIFICITY. MEDLINE=20391985; PubMed=10931875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98220650; PubMed-9562181; Collinson J.M., Marshall D., Gillespie C.S., Brophy P.J.; "Transient expression of neurofascin by oligodendrocytes at of myelinogenesis: implications for mechanisms of axon-glial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during the early stages of myelination.
SUBUNIT: Probable constituent of a neurofascin/NRCAM/ankyrin G
complex. Associates with the sodium channel beta-1 (SCN1B) and
beta-3 (SCN3B) subunits. Associates to beta-1 subunit in
developing axons as early as postanatal day 5, during the period
that nodes of Ranvier are forming. Isoform 2/3 is likely to
interact with axonal proteins in close association with CNTNAP1.
SUBCELIULAR LOCATION: Type I membrane protein. Isoform 1
colocalizes with ankyrin G at the nodes of Ranvier. Isoform 2/3 is
a glial component of the paranodal axo-glial junction.
ALTERNATIVE PRODUCTS:
                                                                                                                                                              L1/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type d
SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                     precipicously.

PTM: Isoform 2/3 is phosphorylated at P12.
required for ankyrin binding.
SIMILARITY: Belongs to the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23:11-23(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       node of Ranvier: identification of
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(See http://www.isb-sib.ch/announce/

86 Usage

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REMBL; U81035; AAB47753.1; -.

REMBL; U81036; AAB47754.1; -.

REMBL; U81036; FN III.

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T -> NNPYNDSSLRNHPDIYSA (in isoform 2 and isoform 3).

FTId=WSP_050417.

Missing (In isoform 3).

/FTId=WSP_050417.

Missing (In isoform 3).

/FTId=WSP_008941.

L -> YERAAPTEVKIRVILNSTAISLOWNRVYPDTVOGQLR EYRAYYWRESSLLKNLWVSQXRQQASFPGDRPRGVVGRLFP YSNYKLEWVVNVGRGDCPRSETKEFTFPEGV (in isoform 2 and isoform 3).

/FTId=WSP_050418.

Missing (In isoform 2 and isoform 3).

/FTId=VSP_050419.

E -> Q (IN REF. 2).

W -> L (IN REF. 2).

W -> YY (IN REF. 2).

G -> Q (IN REF. 2).

G -> YY (IN REF. 2).

G -> YY (IN REF. 2).
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IG-LIKE C2-TYPE 2.
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IG-LIKE C2-TYPE 5
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IG-LIKE C2-TYPE 6
IG
Score 143.5; DB 1;
Pred. No. 0.15;
7; Mismatches 193;
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VLDVPPRMLSPRNQL 439	SLSPGLQL 434	DPLQSAPPNENREVAGDTIIFRDTQISSRAVYQCNTSNEHGYLLANAFVS 424	QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426	GSIRHTISVRVKAAPYWLDEPKNLILAPGEDGRLVCRANG-NPKP-TVQWLVNG 374	APIEKTIS-KAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 370	-PTPDIAWYKKGGDLPSDKAKFENFNKALRITNVSEEDSGEYFCLASNKM 322	DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314	LKVLTTRGVAERTPS-FMYPQGTSSSQMVLRGMDLLLECIASGV 273	IDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254	PVIFWMSSSMEPITODKRVSQGHNGDLYFSNVMLQDMQTDYSCNARFHFTHTIQQKNPFT 230	PSVQCRSPRGKNIQGGKTLSVSQLELQDSGT-WTCTVLQNQKKVEFK 196	ALSNRIRLQVSKSPLWPKENLDPVVVQEGAPLTLQCNPPPGLPS 170	LKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPG-SS 150	NPAPSFHWTRNSRFFNIAKDPRVSMRRRSGTLVIDFRSGGRPEEY-EGEYQCFARNKFGT 126	KKSIQFHW-KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKN 98	PWVHVALILFLLSLGGAIEIPMDPSIQNELTQPPTITKQSVKDHIVDPRDNILIECEAKG 67	PERHLLLYLQLALLPAATQGNKVVLGKKGDTVELTCTASQ 45

Search completed: August 3, 2004, 13:09:30 Job time: 13.0314 secs

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A;Note: this sequence has the GIm(3) marker R;Rutishauser, U.; Cunningham, B.A.; Bennet Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human A;Reference number: A90564; MUID:71064025; A;Contents: Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-1 chain C region - human ($2,500 cts: Homo sapiens (man) C;500 cts: Homo sapiens (man) C;500 cts: Homo sapiens (man) C;500 cts: 31-4an-1931 #sequence revision 18-Aug-1982 #text change 16-Jul-1999 C;Accession: A93431; S36861; $33887; B90563; A90564; B91668; A91723; A02146 R;511ison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 Nicleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432
                                                                                                                A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human
A;Reference number: A90563; MUID:71064024;
A;Contents : myeloma protein Eu
A;Accession: B90563
                                                                                                                                                                                                                                                 A;Title: Structure of human immunoglobulin A;Reference number: S33887; MUID:83001943; A;Accession: S33887
                                                                                                                                                                                                                                                                                           R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, Cell 29, 671-679, 1982
                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $33904
A; Accession: $36861
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A;Residues: 1-330 <ELL>
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the Glm(17) allotypic marker,
A;Note: Lys-330 is removed after translation
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A;Accession: A93433
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;Residues: 88-113;235-330
                                                                                      ;Molecule type: protein
;Residues: 1-96,'R',98-135 <CUN>
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                                                         marker, 9
Bennett,
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                                                                                                                                                                                        Gall, W.E.; Gottlieb,
                gammaG-immunoglobulin. VIII. Amino acid
PMID:5530842
                                                                                                                                                gammaG-immunoglobulin.
PMID:5489771
                                                                                                                                                                                                                                                                gamma genes:
PMID:6811139
                                          97-Arg
, C.; Konigsberg, W.H.; Edelman, G.M.
                                                                                                                                                                                                                                                                                                       T.; Nakai, S.; Honjo,
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F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83;144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;F;20-85/Domain; immunoglobulin homology <IM1;
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A;Rolecule type: protein
A;Rolecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu.
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu.
A;Contents: annotation; disulfide bonds
A;Contents: annotation;
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A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',270,40,000  
A;Residues: this sequence has the GIm(17) and GIm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
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A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
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A; Residues: 136-154, (0',156-165,'(2',167-176,'(2',178-194,'N',196-197,'D',199-238,'E',240,
A; Rote: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
A; Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
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A;Contents: myeloma protein Nie
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ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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                                                                                                                                                                        NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                                                                                                                               NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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74.58;
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Pred. No. 7.1e
7; Mismatches
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7.1e-66;
-heg 22;
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R;Filpula, D.

submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions
A;Reference number: S31866
A;Accession: S31866
                                                                                          Ig gamma-1 chain C region -
C;Species: Bynthetic
A;Note: Homo sapiens (man) g
C;Date: 06-Jan-1995 #sequenc
C;Accession: S31866
                                                                                                                                                                                       RESULT
S31866
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(Species: Homo sapiens (man)
(C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
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A; Residues: 1-140, °C', 142-374 <KH2>
A; Cross-references: EMBL: X81695
C; Superfamily: immunoglobulin C reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Khamlichi, A.A. BMBL Data Library, submitted to the EMBL Data Library, A;Reference number: S72664
A;Accession: S72664
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A; Residues: 1-374 < KHA>
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Best Local Similarity
Matches 242; Conserv
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                                                                                                                                                                                                                                                                                                                                                              VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
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                                                                                                                                                                                                                                                                   SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                        s (man) gene engineered and expressed in Escherichia coli
#sequence_revision 17-Mar-1997 #text_change 19-May-2000
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                                                                                                                                                                     synthetic
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Pred. No. 2
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                                     products.
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A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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A; Residues: 1-234 <EHR>
                                                                                                                                                                                                                                                                                                                                                                           R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee A;Reference number: PT0207; MUID:91287716; A;Accession: PT0207
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma chain C region - chimpanzee C;Species: Pan troglodytes (chimpanzee) C;Date: 23-Nov-1991 #sequence_revision C;Accession: PT0207
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PT0207
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Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                        Matches 221;
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Best Local Similarity
   176
                           367
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                                                                            KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                    VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                      VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
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ESSGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                       KVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEW
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Pred. No. 7.6
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PMID:2062315
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Ig gamma-3 chain C region (allotype G3m (Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence\_revision C;Accession: A23511 R;Huck, S.; Fort, P.; Crawford, D.H.; I

D.H.; Lefranc,

Lefranc,

G3m(b)) -

humar

28-Dec-1987

#text\_change

23-Jul-1999

RESULT A23511

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A;Cross-references: GDB:119339; OMIM:14
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 16
C;Superfamily: immunoglobulin C region;
C;Keyworde: immunoglobulin
F;20-85/Domain: immunoglobulin
                                                                                                                                                                                                 R;HUCK, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
                                                                                                                                                                                                                                                                           Ig gamma-3 chain C region, form LAT - human C;Species: Homo sapiens (man) C;Daccies: Homo sapiens (man) C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999 C;Accession: A60764 R;Huck, S.; Lefranc, G.; Lefranc, M.P.
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A;Title: Sequence of a human immunoglobulin gamma 3 heavy
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A; Residues: 1-377 < HUC>
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A; Residues: 1-377 < HUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A23511; MUID:86148507; A; Accession: A23511
                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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                                                                                                                      Superfamily: immunoglobulin C region; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-85/Domain: immunoglobulin homology <IMM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
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                                  al Similarity
239; Conserv
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 TKGPSKLNDRADSRRS---
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                                                                                                    immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.8%; Score 1157; DB 2; 57.3%; Pred. No. 1.3e-61;
                                                  42.7%;
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                                                  Score 1155;
Pred. No. 1.
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                                              DB 2;
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NYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPG
                        NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELK----TPLGDTTHTCPRCPEP
                                                                                                                                                                                            DPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                      DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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                                                                                              APIEKTISKTKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESSGOPEN
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  376
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A; Molecule type: protein
A; Residues: 1-289 < FRA>
A; Residues: 1-289 < FRA>
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A; Note: the sequence of residues 42-76 was taken from the reference that follows
R; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A; Reference number: A92219; MUID:77118561; PMID:402363
A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A; Accession: A92219 A;Contents: heavy chain disease A;Accession: A90442 Ig gamma-3 heavy chain disease proteins gamma3

A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 901, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corx A; Molecule type: protein A; Residues: 12-97 < MIC> A; Note: the hinge region in idue segment (12-28) gamma-3 chains is about four times , 57, L. 28 long ,69 as in 72 form gamma

A; Accession: A90198

corresponding

ö

residues

zuc.

Structure

A; Molecule type: protein
A; Residues: 59-125, 'BB', 128-226, 228-289 < WOL>
A; Residues: 59-125, 'BB', 128-226, 228-289 < WOL>
A; Note: this protein lacks most of the V region, all of t R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence A; Reference number: A93915, MUID:82247835, PMID:6808505
A; Contents: heavy chain disease protein Omm Frangione, all of the B.; 吕 1 region,
Franklin, and part of , E.C.; Hood, gene

A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Note: a carboxyl-terminal Lys is removed posttranslationally

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A; Note: this seque
C; Comment: The hea
C; Genetics:
A; Gene: GDB: IGHG3
                                                                                                                                                                                                                                                                                                                                  A;Title: The primary structure of a human IgG2 heavy chain: A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'0','21-57,'Z',59,'A',61-193,'D',195-325 <WA;Residues: 1-19,'G',71-15-16 is at or near the complement-binding site R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-2 chain C region - human

(;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heal, Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
E;203-270/Domain: immunoglobulin homology <IMW
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                    A; Molecule type: protein
A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'A
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Reference number: A93132; MUID:80114419; PMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-326 <ELL>
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
                                                                                                                                                                                                                                       A;Title: The amino acid sequences of the three heavy chain A;Reference number: A90752; MUID:80001357; PMID:113060 A;Contents: myeloma protein Zie A;Accession: A90752
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Best Local S
Matches 209
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09; Conservative
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Pred. No. 2.
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PMID:118920
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A;Reference number: A90933
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was derights, J.R.L.; Buttery, S

determined from S.H.; De Vries,

the germline gene G.M.; Milstein, C

A; Title: Nucleotide sequence of a human immunoglobulin A; Reference number: A90933; MUID:83157104; PMID:6299662

C-gamma4

Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #sequence revision C;Accession: A9093; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981

02-Apr-1982

#text\_change 16-Jul-1999

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A;Cross-references: GDB:119338; OMIM:147110

A;Gross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kage) position: An immunoglobulin bome cases, such as IgA and IgM, the subunits associate into lace; Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85;Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;133-202/Domain: immunoglobulin homology <IM3>
F;147/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83;140-200;246-304/Disulfide bonds: #status experimental
F;102;103;106;109/Disulfide bonds: interchain (to harange predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Milstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
A;Contents: number; Pink, JR.L.
Nature 221, 145-148, 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, Marc
A;Reference number: A94591
A;Contents: annotation; Zie,
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Best Local
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                                                                                                                                                                         VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC
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MHEALHNHYTOKSLSLSPG
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82.6%;
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325
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Pred. No. 4e-6
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PMID:5782707
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60-Ala and
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N;Alternate names: T-cell surface antigen T4/Leu J
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence revision 31-Dec-1988 #text change 20-Apr-2001
C;Dates: 28-May-1986 #sequence revision 31-Dec-1988 #text change 20-Apr-2001
C;Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039
R;Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, F
Cell 42, 93-104, 1985
A;Title: The isolation and nucleotide sequence of a cDNA encoding the T cel:
A;Reference number: A90872; MUID:85254948; PMID:2990730
A;Accession: A90872
                                                      Cell
                                                                            Cell 55, 541, 1988
A;Title: Corrected CD4 sequence.
A;Reference number: A90907; MUID:89028665; PMID:3263213
A;Contents: annotation; revision to residue 26
R;Camerini, D; Seed, B.
                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-25,'N',27-458 <MAD>
A;Experimental source: clone pT4B
R;Littman, D.R.; Maddon, P.J.; Axel,
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (bo light chain) #status experimental F;27-83,141-201,247-395/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IMI>F;99-110/Region: hinge
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A;Map position: 14932.33-14932.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell surface glycoprotein CD4 precursor [validated] - N;Alternate names: T-cell surface antigen T4/Leu 3
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A; Residues: 1-30;81-326 < PIN>
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A;Accession: A90249
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A:Reference number: A90249; MUID:70207560;
     A; Reference number: A32722;
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;Title: A CD4 domain important for HIV-mediated syncytium formation;Reference number: A32722; MUID:90182664; PMID:2107024
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83.7%;
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

180

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A;Molecule type: mRNA
A;Residues: 26-426,428-458 <CAM>
R;Carr, S.A.; Hemling, M.E.; Folena-Wasserman,
J. Biol. Chem. 264, 21286-21295, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 14, 590-597, 1992
A;Title: A human dimorphism resulting from loss of an Alu.
A;Reference number: I54176; MUID:93052387; PMID:1330888
A;Accession: I54176
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A;Title: A single amino acid substitution in a common African allele of the CD4 molecule A;Reference number: A53287; MUID:92072595; PMID:1961196
A;Accession: A53287
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A;Residues: 26-394 <CAR>
R;Lederman, S.; DeMartino, J.A.; Daugherty, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 264, 21286-21295, 1989
A;Title: Protein and carbohydrauterotural analysis of A;Reference number: A34194; MUID:90078232; PMID:2592374
A;Contents: disulfide bonds; carbohydrate-binding sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: sequence extracted f
R; Edwards, M.C.; Gibbs, R.A.
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A;Status: nucleic a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119767; OMIM:186940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: GDB:CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-264,'W',266-458 <RE2>
A;Cross-references: GB:M35160; NID:g179143; PIDN:AAA16069.1; PID:g179144
C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-72 <RES>
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A; Residues: 250-264, 'W', 266-280 <LED>
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A;Molecule type: pro
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                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology; Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein; 1-25/Domain: signal sequence #status predicted <SIG>
7.26-458/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
7.34-111/Domain: immunoglobulin homology <IM1>
7.136-186/Domain: immunoglobulin homology *IM1>
7.136-186/Domain: immunoglobulin homology #status atypical <IM2>
7.136-299/Domain: immunoglobulin homology <IM3>
7.216-299/Domain: immunoglobulin homology <IM4>
7.321-372/Domain: immunoglobulin homology <IM4>
7.321-372/Domain: transmembrane #status predicted <IMM>
7.397-420/Domain: transmembrane #status predicted <IMT>
7.41-109,155-184,328-370/Disulfide bonds: #status experimental
7.41-109,155-184,328-370/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          Local
                           121
                                                                                    61
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQ1K
                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                                                                                                                             37.9%;
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Pred. No. 1.
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..5e-53;
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A; Molecule type: DNA
A; Residues: 1-398 <WEL>
A; Residues: 1-398 <WEL>
A; Residues: 1-398 <WEL>
A; Residues: GB:J00451; NID:g194392; PIDN:AAB59655.1; PID:g194433
A; Cross-references: GB:J00451; NID:g194392; PIDN:AAB59655.1; PID:g194433
A; Note: the sequence was determined from the germline gene
R; Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R
Nucleic Acids Res. 11, 6775-6785, 1993
A; Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene
A; Reference number: A02155; MUID:84041483; PMID:6314258
A; Accession: A02155
A; Accession: A02155
A; Molecule type: DNA
A; Residues: 328-332 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
A; Residues: 328-332 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
A; Rosidues: 38-332 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Introns: 97/1; 113/1; 223/1; 328/1; 371/3
C; Complex: An immunoglobulin heterotetramer subunit consists of two identica
G1MSM
Ig gamma-1
C;Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kal hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1. C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuf; 19.83/Domain: immunoglobulin homology <IMI>
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C;Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text
C;Accession: A02156; A02155
R;Wells, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Mar
EMBO J. 3, 2041-2046, 1984
A;Title: Structure analysis of the murine IgG3 constant
A;Reference number: A02156; MUID:85027161; PMID:6092053
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A; Molecule type: DN
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Best Local S
Matches 180
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;363-398/Domain: intracellular #status predicted <INT>
;179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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  chain C region, memb
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                                                                                                                                                                                              SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
                                                                                                                                                                                                                                                                       REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT
                                                                                                                                                                                                                                                                                                                         RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                                 QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGPSVPIFPPXPXDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
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                                                                                                                                                               DSWLQGE1FTCSVVHEALHNHHTQKNLSRSPELELNETCAEAQDGELDGLWTT
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                              mouse
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C;Date: 17-Dec-1982 **BEQUARTION C;Accession: 802159; A02160; B02158 R;Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide se A;Title: Cloning And Complete NUID:80045036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;131-200/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A02160; MUID:82197626; PMID:6804950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: this sequence is the translation of the first exon of the M segment C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ncode membrane-bound chains in that it contains an alternative 3' end, encoded in sepandode membrane-bound chains in that it contains an alternative 3' end, encoded in sepandode membrane
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A;Residues: 323-393 <TYL>
R;Rogers, J.; Choi, E.; Souza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the sequence was determined from the germline R;Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
A;Title: mRNA for surface immunoglobulin gamma chains
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A; Residues: 323-366 < ROG>
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A; Residues: 1-393 < HON>
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323
                                                                                                                                                                                                              311 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQ
                                                                                                                                                                                                                                                                                                                                                                 91 TKVDKKIVPRDCGC-KPCIC----TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 VLQSDLYTLSSSVTVPSSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                 KKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVD
                                             GLQLDETCAEAQDGELDGLWTT 452
                                                                                       QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
                                                                                                                             QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                               AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG
                                                                                                                                                                                                                                                                         ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS
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Pred. No. 2.9e-48;
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Ig heavy chain precursor (B/MT.4A.17.H5.A5) . N;Alternate names: Ig gamma-1 chain C region C;Species: Bos primigenius taurus (cattle)

(clone

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C;Date: 06-Jan-
C;Accession: S2
R;Sanders, P.G.
Ig gamma-2a chain C region, membrane-bound form -
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 31-Mar-1991
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin; membrane protein
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X62916; NID:g439; P
R;Symons, D.B.A; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin
A;Reference number: S06610; MUID:90097956; P
A;Accession: S06610
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A; Residues: 142-470 <SYM>
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
A; Note: the sequence was determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A;Accession: S22080
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                                                                                                                                                                                                                    AVEWQRNGQPESEDKYGTTPPQLDADSSYFLYSKLRVDRNSWQEGDTYTCVVMHEALHNH
                                                                                                                                                                                                                                                                                                   EFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPPQEELSKSTVSLTCMVTSFYPDYI
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                                                                                                                                          YTQKSTSKSAG
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#sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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Pred. No. 3.7e-47;
2; Mismatches 136;
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Ig gamma 2a chain constant region - pig C;Species: Sus scrofa domestica (domestic;jatte: 21-Feb-1997 #sequence_revision 2;Accession: I47159 R;Kacskovics, I.; Sun, J.; Butler, J.E. J. Immunol. 153, 3565-3573, 1994
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A;Residues: 373-399 <RES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma hat it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the sequence was determined from the germline gene R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: B32657
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C;Complex: An immunogiobulin heterotetramer subunit consists of two ide
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A;Title: Sequence and polyadenylation site determination of the murine immunoglobulin A;Reference number: I57809; MUID:90097953; PMID:2513486
A;Accession: I57809
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A;Cross-references: GB:J00471
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I.; 5u..,
53, 3565-3573,
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                                                                                                                                                                                                                                                                                                                                                                                                                     VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
                                                                                                                                                                                                                                                                               SYSCSVVHEGLHNHHTTKSFSRTPGLDLDDVCAEAQDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELLGGPSVF 226
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21-Feb-1997
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A; Molecule type: mRNA
A; Residues: 1-323 <BER>
A; Note: this sequence has the dl2 allotypic m
R; Pratt, D. M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant reg
A; Reference number: A90290; MUID: 76135469; PM
A; Accession: A90290
A; Molecule type: protein
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-328 <KAC- A;Crqss-references: EMBL:U03779; NID:g433123; PIDN:AAA5221 C;Genetics: A;Grqs: immunoglobulin C region; immunoglobulin homology <IMM's
A; Molecule type: protein
A; Residues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
A; Residues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
A; Residues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
A; Refidues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
A; Refidues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
A; Refidues: C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy Chain genes of rabbit 1gG; isolation of a cDNA encoding gamma heavy chain A; Title: Heavy Chain genes of rabbit 1gG; isolation of a cDNA encoding gamma heavy chain A; Accession: A93928
A; Accession: A93928
A; Molecule type: mRNA
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic marker
B; Fruchter, R.G., Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma chain C region - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus revision 15-Nov-1984 #C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #t C;Accession: A91749; A90290; A93928; A90245; A94416; R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
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Best Local S
Matches 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVEWESNGQ -- PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATTTKVDKRVGTKTKPPCP-----ICPACESPGPSVFIFPPKPKDTLMISRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKVEFKID-----IVPCPAPEPKSCDKTHTCPELLG-GPSVFLFPPKPKDTLMISRTP
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58.5%;
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Pred. No. 1.7e
38; Mismatches
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                                                                                                                                                                                                                                                                                                                                          region of the PMID:1243651
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6; A02161
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3555-3573, 1994
A;Title: Five putative subclasses of swine
A;Reference number: I47158; MUID:95015845;
A;Accession: I47162
A;Status: preliminary; translated from GB/E
A;Molecule type: mRNA
A;Residues: 1-277 < KAC>

A;Gene: IgG4 C;Superfamily: i F;82-151/Domain:

immunoglobulin C

region; immunoglobulin homology
homology <IMM>

immunoglobulin

A;Cross-references: C;Genetics:

EMBL: U03782;

NID:g433129;

PIDN:AAA52220.1;

PID: 9433130

GB/EMBL/DDBC

IgG identified PMID:7930579

from

the

cDNA sequences

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#text\_change

21-Jan-2000

S

168

Query Match Best Local S Matches 172

Local Similarity

33.2%; llarity 62.8%; Conservative 3

Score 898; DB Pred. No. 2.1e 33; Mismatches

2.1e-46;

Length 277

Indels

26;

Gaps

6

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19

TVPASSL---SSKSYTCNV--NHPATTTKVDKRVGTKTKPPCP-

ICPACE

62

220

TLSVSQLELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELL

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A,Reference number: A94416
A;Accession: A94416
A;Accession: Complex: Ap4416
A;Accession: A94416
A;Accessio
Ig gamma 4 chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 C;Accession: I47162 R;Kacskovics, I.; Sun, J.; Butler, J.E. J. Immunol: 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin E;20-82/Domain: immunoglobulin homology <IM1>
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R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R. in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-1
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                                                                                                                                                                                                                                                                                                                                                                                                       TLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEK
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Pred. No. 2.2e
34; Mismatches
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.2e-46;
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RESULT 19
G2GP
           Ig gamma-2 chain C region - guinea pig (;Species: Cavia porcellus (guinea pig) C;Bpecies: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence revision 07-May-1981 #text_che C;Accession: A94553; A90352; A90359; A90384; A90385; A02151 C;Accession: T.M. submitted to the Atlas, April 1975 A;Reference number: A94553
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A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin
F:133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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A; Accession:
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A; Residues: 1-328 < KAC>
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A;Title: Five putative subclasses of swine
A;Reference number: 147158; MUID:95015845;
A;Accession: 147160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: I47160
R; Kacskovics, I.; Su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                             DKASWOGGGI FOCAVMHEALHNHYTOKS I SKTPG
                                                                                                                                                                                                                                                          AEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSV
                                                                                                                                                                                                                                                                                     RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 898; DB 2;
Pred. No. 2.6e-46;
                                                                         07-May-1981 #text_change
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                                                                            16-Jul-1999
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A,Residues: 134-226 <TRA>
R,Trischmann, T.M.; Cebra, J.J.
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295
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VDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG
                                                                                                                                                                                                                                                                                                                        Conservative
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A;Molecule type: protein
A;Residues: 227-311 cTR2>
R;Oliveira, B:; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-16; Cys-107, and Cys-10 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Comment: This chain was isolated from pooled serum of strain and inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology city.
F:131-304/Domain: immunoglobulin homology city.
F:131-304/Domain: immunoglobulin homology city.
F:131-304/Domain: immunoglobulin homology city.
F:131-304/Domain: immunoglobulin homology city.
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Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region !
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
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A; Residues: 69-133;312-329 <TUR>
R; Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A; Title: Primary structure of the C-H2 homology region 1
A; Reference number: A90384; MUID:75036072; PMID:4429665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;135-204/Domain: immunoglobulin homology <IM2>F;241-310/Domain: immunoglobulin homology <IM3>F;248-79/Disulfide bonds: #status experimental F;142-202/Disulfide bonds: #status experimental F;178/Binding site: carbohydrate (Asn) (covalent) F;248-308/Disulfide bonds: #status experimental
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A;Residues: 1-3 <TRI>
R;Birehtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
B;Title: Structure of heavy chain from strain 13 guinea
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
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Biochemistry 10, 9-17, 1971
A;Tille: Structure of heavy chain from strain 13 guinea
A;Reference number: A90359; MUID:71058486; PMID:5538616
                                                                                                                                                                                                                                                                                                                                                                                    NLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
                       VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                            SRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLT
                                                                                                                                                   SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLT 396
                                                                                                                                                                                                                                                     EQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPP
                                                                                                                                                                                                                                                                                             EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOSGLYSLTSMVTVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPCTCPK---CPPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKVEFKIDIVFCPAPEFKSCDKTHTC--PE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.1%; Score 894.5; DB 1 62.5%; Pred. No. 4.2e-46;
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine
A; Reference number: 147158; MUID:95015845;
A; Accession: 147158
                                                                                                                                                                                                                                                                                                                                               RESULT
G2MSBM
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C;Superf
                                                  A;Title: Gene segments encoding transmembrane carboxyl termini A;Reference number: A02158; MUID:82115295; PMID:6799207 A;Accession: A02158
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A; Residues: 1-328 < KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma 1 chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-199 C;Accession: I47158
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 335-405 < YAM>
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                                                                                                                                                                                                                                                                           Ig gamma-2b chain C region, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change
C;Accession: C02154; A02158; B02157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 180
                ,Molecule type: DNA
,Residues: 335-378 <ROG>
                                                                                                    ;Cross-references: GB:J00462
;Rogers, J., Choi, E.; Souza, L.;
ell 26, 19-27, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;133-202/Domain:
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   tranglation of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGSSPSVQCRSPRGKNIQGGKT----LSVSQLELQDSGTWTC-----TVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDGTFFLYSKLAVDKARWDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin C region; immunoglobulin homology
in: immunoglobulin homology <IMM>
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#ведиепсе_revision 21-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.5%; Score 879.5; DB 2
55.2%; Pred. No. 3.3e-45;
tive 38; Mismatches 67
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C;Species: Pan troglodytes
C;Date: 30-Sep-1993 #sequen
C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A;Molecule type: mRNA
A;Residues: 1-432 <CAM's
A;Cross-references: GB:M31135
A;Cross-references: GB:M31135
Bur. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules:
A;Reference number: A46534; MUID:93049640; PMID:1425921
A;Accession: A46534
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin C region; immunoglobulin homolo C;Keywords: alternative splicing; duplication; glycoprotein; F;143-212/Domain: immunoglobulin homology <IMM> F;352-369/Domain: transmembrane #status predicted <INM> F;370-405/Domain: intracellular #status predicted <INT>
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A;Residues: 1-335,'K' <YA2>
C;Comment: The sequence of residues 1-334 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The mahat it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                        A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024 A;Accession: B32722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Complete nucleotide sequence of immunoglobulin A; Reference number: A02157; MUID:80120716; PMID:6766534
                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell surface glycoprotein CD4 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;186/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                    ;Species: Pan troglodytes (chimpanzee);Date: 30-Sep-1993 #text_change 16-Jul-1999;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TCTVLQ--NOKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCNVRHEGIKNYYLKKTISRSPGLDLDDICAEAKDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.5%; Score 877.5; DB 1;
51.7%; Pred. No. 5.5e-45;
52. Mismatches 75;
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antigen T4/Leu
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A;Residues: 3-399 <FOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
C;Comment: This protein is expressed on most thymocytes, on a subset of mature (Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication, glycoprotein; T-cell; transmembrane protein P;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-371/Domain: extracellular #status predicted <EXT>
F;9-86/Domain: immunoglobulin homology <IM1>
F;111-161/Domain: immunoglobulin homology *IM3>
F;296-347/Domain: immunoglobulin homology <IM3>
F;396-347/Domain: transmembrane #status predicted <TMM>
F;392-395/Domain: transmembrane #status predicted <TMM>
F;396-432/Domain: intracellular #status predicted <INT>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
C;Accession: 147161
R;Kacskovics, I:; Sun, J:; Butler, J.E.
J. Immunol, 153, 3565-3573, 1994
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A; Residues: 1-328 < KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Five putative subclasses of swine A;Reference number: I47158; MUID:95015845; A;Accession: I47161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133-202/Domain:
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Best Local
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197
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EFKCKVNNVDLPAPITRTISKAIGOSREPOVYTLPPPAEELSRSKVTVTCLVIGFYPPDI
                                          EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI 362
                                                                                                                                       EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 302
                                                                                                                                                                                         PATTTKVDKRVGTKTKPPCP------ICPGCEVAGPSVFIFPPKPKDTLMISQTP
                                                                                                                                                                                                                                      KKVEFKID-----IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTP 242
                                                                                                                                                                                                                                                                                        EPVTMTWNSGALTSGVHTFPSV--LQPSGLYSLSSMVTVPASSL---SSKSYTCNV--NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDQGNFTLTIKNLKIEDSDTYICEVGDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                32.3%; Score 873; DB 2
57.6%; Pred. No. 8e-45;
vative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%;
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Pred. No. 8.4e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                     61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu C;KeyBondin: immunoglobulin homology <IMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-3 chain C region, secreted form - mouse (;Species: Mus musculus (house mouse) C;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: B02156 R;Accession: B02156 R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, ENBO J. 3, 2041-2046, 1984 The murine IgG3 constant region gene. A;Fitle: Structure analysis of the murine IgG3 constant region gene. A;Reference number: A02156; MUID:85027161; PMID:6092053
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C; Complex:
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A; Residues: 1-329 <WEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;179,322/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;136-205/Domain: immunoglobulin homology <IM2>F;242-309/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J00451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B02156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                              400
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RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                                                        SVSQLELQDSGTW-----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP--EL 219
                                                                                           REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT 296
                                                                                                                                                                               QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
                                                                                                                                                                                                        QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                     LGGPSVFIFPPKPXDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
                                                                                                                                                                                                                                                                                                                 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                                                                                                                                                                                                                                                                                                                                                              SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS----SCPPGNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.7%; Score 857.5; DB 1 59.6%; Pred. No. 6.7e-44;
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Peb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; K
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody

H.; Kamachi, M.; Harada,

P

13-1 against

porphyr

21-Jan-2000

PC4436

25

A; Reference number: JC5810; MUID: 98063277; PMID: 9398605 A; Accession: PC4436

;Molecule type:

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K;Patri, S31459

K;Patri, S; Nau, F.

Submitted to the EMBL Data Library, December 1992

A;Reference number: S31459

A;Accession: S31459

A;Accession: S31459

A;Residues: preliminary

A;Molecule type: mRNA

A;Residues: 1-472 <PAT>

A;Cross-references: EMBL:X69797

C;Superfamily: immunoglobulin C

C;Keywords: immunoco
                                                                                                                                                                                                                                                                                                                                                      RESULT 26
$31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis
C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S31459
R;Patri, S; Nau, F
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Best Local S
Matches 196
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Best Local S
Matches 188
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                                                                                                                                                                                                            Superfamily: immunoglobulin C region; immunoglobulin; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399
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This catalytic antibody has peroxidase oxidase activity. It is
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                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS--GSLSSGVHTFPA---VLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIS-RDDSKSSVYLOMN-----RLREEDTATYYCCRTPWVYAMDCWGQGTSVIVSSAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKIL-----GNQGSFLTKGPS
                                                                TLSVTCTISGFSLNNYGVDWVRQAPGKALEWLGGSGYDEDIDYNPVLKSRLSITKDTSKS
                                                                                              TVELTCTAS--QKKSIQFHWKN---SNQIKILGNQG--SFLTKGP---SKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGC-KPCIC----TVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKEEVQLLVFGLTANSDTHLLQG------QSLTLTLESPPGSSPSVQCRSPRGKNIQG
   ----QVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWGPGLLISVLSAST----
                                 LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE-----VQLLVFGLTANSDTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKTLSVSQLELQDSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC-----EVED
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                                                                                                                                              31.6%;
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41.5%; Pred. No. 1.4e-43;
tive 76; Mismatches 118;
                                                                                                                              Score 854.5; DB 2; Pred. No. 1.5e-43; 55; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: S37483
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Matches 197
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   329
                                                               269
                                                                                                                              209
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                                                                                                                                                                                                                                                         LTLTLESPPGSSPSVQ-----CRSPRGKNIQGG-----KTL------KTL
                                                                                                                                                                                                                                                                                                                                                      LVKPGASVKISCKASGYTFTDYY---INWVKQKPGQGLKWIGWIYPASGNTKYNENFKGK
REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                                                                                             KC----PAPNILGGESVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE
                                                                                                                  SCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                      RSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQS
                                 VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV
                                                 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                            PAVLOSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---PC
                                                                                                                                                                                          -SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPK 208
                                                                                                                                                                                                                        TILIVSSAKTIAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVILIWNSGSLSSGVHTF
                                                                                                                                                                                                                                                                                        ATLTVDTSSSTAYMQLSSLTSEDTAVYFC------ARAMGATAT----LLDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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428	388	368	330	308	270	251	212	194	174	145	134
SYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPG 471	SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	EPQVYVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADG 427	330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387	RTARTKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAR 367	270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329	RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEV 307	212 KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269	FPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVE-PGCPDP-CKHC- 250	174 LELODSGTWTCTVLQNOKKVEFKIDIVPCPAPEPKSCD 211	TPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVHT 193	134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNI

A;Molecule type: mRNA
A;Residues: 1-469 <DUC
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1;
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM> Ig gamma-2a chain - mouse
(;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence\_revision
C;Accession: \$37483
R;Ducancel, F.F.D. 30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR 31.5%; Library, 56; Score 850.5; DB 2 Pred. No. 2.7e-43; 6; Mismatches 125 February 06-Jan-1995 #text\_change 23-Jul-1999 1993 125; 2 Indels Length homology 469; PID: 9406253 85; Gaps 83

365

328 305 268

249

169

138 86

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A; Molecule type: DNA
A; Residues: 1-333 < BRU>
A; Residues: 1-333 < BRU>
R; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking A; Reference number: AZ5941; MUID:86287397; PMID:3016742
A; Accession: BZ5941
                                                                                                                                                                           A;Title: Evolution of the r
A;Reference number: PS0017;
A;Accession: PS0018
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C;Accession: PS0018; B25941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711
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C; Accession: C30554
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A; Molecule type: DNJ
A; Residues: 227-333
                                 A; Status: preliminary
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                                                                                                                                                                                                                                                    R;Brueggemann,
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;113-182/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                      gamma-2b chain C region - rat
Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Ovis orientalis aries, Ovis ammon aries pate: 03-Mar-1989 #sequence_revision 03-Mar-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y heavy chain C region - sheep (fragment);Species: Ovis orientalis aries, Ovis amm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                   473-482, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVTVPASTSGAQTFICNVAHPASSTKVDKRVE-PGCPDP-CKHC----RCPPPELPGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQVYVLAPPQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTARTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVSQLELQDSG--TWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTC--PELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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 <BR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%;
60.7%;
                                                                                                                                                                                               rat immunoglobulin gamma heavy-chain 7; MUID:89232738; PMID:3149946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 838;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                         07-Jun-1990
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#text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                     #text_change 16-Jul-1999
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                                                                                     homology to
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                                                                                                                       Waldmann,
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                                                                                       mouse
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F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <VDJ>
F;118-244/Domain: C region <CH1>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
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                                                                                                                                                                                                                                                                    F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted F;122/Disulfide bonds: interchain (to light chain) #status predicted F;122/Disulfide bonds: interchain #status predicted F;224,227,229/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molécule type: protein A;Residues: 1-446 <KLE> C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bsubmitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-Za chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision
C;Accession: S40295
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                       F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S40295
A; Accession: S40295
                                                                                                                                                                                                                                                 ;297/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                        Query Match
Best Local
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Best Local Similarity
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                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
GKATLTVDTSSSTAYMQLSSLTSEDSAVYFC---
                                       SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G
                                                                                                                       LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGTW-----TCTVLQ--NQKKVEFKIDI-----VPCPAPEPKSCDKTHTC--PELLGGP
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                    30.5%;
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58.6%;
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                                                                                                                                                                                    Score 825; DB 2;
Pred. No. 8.2e-42;
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Pred. No. 1.
                                                                                                                                                                  Mismatches 123;
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1.9e-42;
53;
                                                                                -VKQRPGEGLEWIGWIYPGSGNTKYNEKFK 65
                                                                                                                                                                                                       Length 446;
                                                                                                                                                                  Indels
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  ARGGKFAMDYWG
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Ig gamma-1 chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07
C;Accession: PS0017; C25941
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C;Genetics:
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A; Residues: 1-326 <BRU>
A; Residues: 1-326 <BRU>
R; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking A; Reference number: A25941; MUID:86287397; PMID:3016742
A; Accession: C25941
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 163; Conser
                                                                                                                                                                                                                                                                                                                       ;Superfamily: immunoglobul
;Keywords: immunoglobulin
;20-84/Domain: immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
                                                                                                                                                QTVTCNVAHPASSTKVDKKI-----VPRNC---
                                                                                                                                                                                                                                  LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFPAVLOSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---
   NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                         RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                                                                                     FIFPKFKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTF
                                                                                                                                                                                                        LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LQSGLYTLTSSVTV-PSSTWPS
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                                                                                                                                                                          -TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG------PSV
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                                                                                                                                                                                                                                                             30.5%; Score 823.5; DB 2; 50.0%; Pred. No. 6.9e-42; tive 53; Mismatches 55;
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A;Title: Immunoglobulin gamma-1 heavy chain gene: structural A;Reference number: A26234; MUID:80202559; PMID:6769752 A;Contents: MOPC 31C A;Accession: A26234
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A;Accession: A02159
A;Molecule type: DNA
A;Residues: 1-324 <HON>
A;Cross-references: GB:J00453
A;Cross-references: GB:J00453
A;Note: the sequence was determined from the germline
A;Note: Lys-324 is removed posttranslationally
R;Obata, M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kata
Gene 9, 87-97, 1980
                                                                                                                                                                                                                     R;HOnjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, Cell 18, 559-568, 1979.

A;Titla: Cloning and complete nucleotide sequence of mouse immunoglobulin gammal ch. A;Reference number: A02159; MUID:80045036; PMID:115593
                                                                                                                                                                                                                                                                                                                          Ig gamma-1 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1980 #sequence revision 24-Sep-1981 C;Accession: A02159; A26234; A26236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiBrueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, F.
Bur. J. Immunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant re
A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847; mRUID:88166903; PMID:3127222
A;Accession: S00847; mRUID:88166903; PMID:3127222
A;Molecule type: mRNA
A;Residues: 1-329 <BRU>
A;Residues: 1-329 <BRU>
A;Cross-references: EMBL:X07189; NID:957602; PIDN:CAA30169.1; PID:g663228
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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58.5%;
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No. 7.5e-42;
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                                               N.; Kataoka,
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Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Jate: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 01-Dec-2000 C;Jate: 31-mar-1980 #sequence revision 01-Dec-2000 #sequence revision for Science for five fields for fields fields for fields for
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F;237-304/Domain: immunoglobulin homology <IM2>
F;237-304/Domain: immunoglobulin homology <IM2
F;237-82,138-198,244-302/Disulfide bonds: #status experimental
F;102/Disulfide bonds: interchain (to light chain) #status experimental
F;104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuf; 20-18/Domain: immunoglobulin homology <IMI>
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A;Contents: annotation; MOPC 21
A;Note: this is the final paper in a series reporting the protein sequence, A;Note: there are a number of differences from the sequence shown
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A;Residues: 170-275,'D',277,'D',279-322 <ROG>
A;Cross-references: GB:V00795; NID:951830; PIDN:CAA24176.1;
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Nucleic Acids Res. 6, 3305-3321, 1979
A;Title: Sequence analysis of cloned cDNA encoding part of an A;Reference number: A26236; MUID:80012837; PMID:113776
A;Contents: MOPC 21
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A;Cross-references: GB:V00775; NID:g51652; PIDN:CAA24153.1;
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                                                                                                                                       H.J.; Kreuzaler,
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;157-222/Domain: immunoglobulin homology <IM1>
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A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUl>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner,
Science 206, 1303-1306, 1379
A;Title: Sequence of the cloned gene for the constant region of A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
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A;Title: Structure of the constant and 3' unt A;Reference number: A26235; MUID:80081501; PM A;Contents: MPC 11
                                                                                                                                                                                                                                                                            F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status
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A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
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A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele s
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A;Residues: 138-161, 'L',163-189,'FP',193-474 <YAM:
A;Cross-references: GB:J00461
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
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A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A;Cross_references: GB:J00461
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A; Accession: A02157
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                                                                                                                                                                                                                                                                                                                                                                                                               ;236-257/Region: hinge
;281-350/Domain: immuno
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                                                                                                                                                          Similarity
GASVKMSCKASGYTFITYVMHW-----VKOKPGQGLEWIGYINPNKDGTKFNEKFKGKAT
                                                              GDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG----SFL--TKGPSKLNDRADSRRS
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Y.; Masuda, K.;
19350, 1994
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                                                                                                                                                      30.3%;
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                                                                                                                         Score 818; DB 1; Length 474; Pred. No. 2.3e-41; 6; Mismatches 124; Indels
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LW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142

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Ig gamma-2a chain c region, consider the manuschild (house mouse)
C;Date: 30-Sep-1980 #sequence revision 01-Sep-1981
C;Date: 30-Sep-1980 #sequence revision 01-Sep-1981
C;Accession: A02152; A32657; A32658
R;Sikorav, J.L.; Auffray, C.; Rougeon, F.
Nucleic Acids Res. 8, 3143-3155, 1980
A;Title: Structure of the constant and 3' untranslation of t
                                                                                                                                                                                                                                                                   A;Residues: 1-330 <OLL>
A;Note: the sequence was determined from the germline gene
A;Note: Lys-30 is removed posttranslationally
R;Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Bur. J. Biochem. 43, 423-435, 1974
A;Title: Determination of the primary structure of a mouse
A;Reference number: A32659; MUID:74175517; PMID:4831970
                         A;Contents: annotation; myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence;
A;Note: this sequence differs from
R;de Preval, C.; Fougereau, M.
Eur. J. Blochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gam
A;Reference number: A32660; MUID:73056887; PMID:4565406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence was determined from the germline gene R;0110, R.; Auffray, C.; Morchamps, C.; Rougeon, F. Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 191 A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes A;Reference number: A32658; MUID:81223894; PMID:6787604
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R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: A32657
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A; Accession: A02152
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A; Residues: 1-330 < YAM>
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annotation;
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MOPC 173,
   disulfide
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 118-267; YE, 269-228; G', 330-334 < DOG>
C; Comment: Iye-335 is removed posttranslationally.
C; Comment: The sequence differs from that of the a allele, from BALB/c mice, at 15% of t C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology < IM2>
F; 98-118/Region: hinge
F; 142-211/Domain: immunoglobulin homology < IM2>
F; 142-211/Domain: immunoglobulin homology < IM2>
F; 142-211/Domain: immunoglobulin homology < IM2>
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Seywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; 20.84/Domain: immunoglobulin homology <IM1>
F;98-113/Region: hinge
F;98-113/Region: hinge
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G2MSAB
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Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
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F:243-510/Domain: immunoglobulin homology <IM2>
F:243-510/Domain: immunoglobulin homology <IM3>
F:15/Disulfide bonds: interchain (to light chain) #status experimental
F:27-82.144-204,250-308/Disulfide bonds: #status experimental
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J00479
A;Experimental source: strain C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A02153; A; Accession: A02153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A;Title: Multiple differences between the nucleic acid sequences A;Reference number: A02153; MUID:82037861; PMID:6170065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
C;Accession: A02153; A32656
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                           ;248-315/Domain: immunoglobulin;15/Disulfide bonds: interchain
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Pred. No. 8.2e-41;
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Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-475 < DE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S01321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                  Query Match
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                                    172
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 193
                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 LELQDSGTW-----TCTV-----LQNQKKVEFKIDIV--PCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GLTANSDT--HLLQG---QSLTLTLESPPGSS----PSVQCRSPRGKNIQGGKTLSVSQ
                                                                                                                                                                          82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                              29.4%; Score 793.5; DB 2; Similarity 40.0%; Pred. No. 6.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                   TLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                     LTLTLESPPGSSPSVQ----CRSPRGKNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELTKNQVSLTCLVXGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                      GKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA---GPRQVGLLPFG-----YWGQG 132
                                                                                                                                                                      SRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                                                                                                                                             LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD 81
PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCP---
                                                                                                                                                                                                          LARPGASVKLSCKASGYTLTSYGISW-----VKORTGOGLEWIGEIYPGSGNSYFNEKFK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWERGSLFACSVVHEVLHNHLTTKTISRSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLRVQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLPPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCP---PHQRVPPCAAPDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAL-----LOSG-LYTLSS
                                                                                                                                                                                                                                                                                 Conservative
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                              SQLELQDSGTW----TCTVLQ--NQKKVEFKID-----IVPCPAPE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.6%;
                                                                                                                                                                                                                                                                              58; Mismatches 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 801; DB 1;
Pred. No. 1.5e-40;
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                                                                                                     QGGKTLSV--- 171
                                                                                                                                                                                                                                                                              87;
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A; Molecule type: DNA
A; Residues: 216-322 <BR2>
C; Genetics:
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C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990
C;Accession: PS0019; D25941
R;Bruecdemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 98/1; 109/1; 216/1
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: D25941
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain
A;Reference number: PS0017; MUID:89232738; PMID:3149946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Brueggemann,
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A; Residues: 1-322 < BRU>
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Best Local
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308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS0019
                                                                                                                                                                                                                                                                                      | ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                               LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LOSGLYTLTSSVTV-PSSTWSS
                                                                                                               YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 417
                                                                                                                                                                                                      WLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGF
                                                                                                                                                                                                                                                                                                                                                    QAVTCNVAHPASSTKVDKKIVPREC---NPCGCTGSEV-----SSVFIFPPKTKDVLT 127
                                                                                                                                                                                                                                                                                                                                                                                 ---TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
HNHHTEKSLSHSPG
                                      HNHYTQKSLSLSPG
                                                                                  YPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKETWQQGNTFTCSVLHEGL
                                                                                                                                                                        WINGKTFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTMAPPKEEMTQSQVSITCMVKGF
                                                                                                                                                                                                                                                             ITLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.3%; Score 792.5; DB 2;
51.0%; Pred. No. 4.7e-40;
47. Mismatches 72;
                                      431
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A;Accebbium.
A;Molecule type: DNA
A;Residues: 1-327 <SYM>
A;Cross-references: EMBL:X16702
A;Cross-rha sequence was determined
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C;Comment: This protein is expressed on most thymocytes, on a subset of C;Comment: This protein is expressed on most thymocytes, on a subset of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication, glycoprotein, T-cell; transmembrane protein F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT> F;1-371/Domain: extracellular #status predicted <EXT> F;9-86/Jomain: immunoglobulin homology <IM1>
                                                                                                                                                                                             A; Gene: Ig CH gamma
A; Introns: 99/1; 11;
                                                                                                                                                                                                                                                A; Note: the sequence was C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: S06611
                                                                                                                                                                                                                                                                                                                                                                                          R;Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-950, 1989
A;Title: Structure of bovine immunoglobulin A;Reference number: S06610; MUID:90097956; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2 chain C region (clone 32.2) - bovine (fragment) C;Specides: Bos primigenius taurus (cattle) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change C;Accession: S06611; B31303
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F;180-293/Domain: immunoglobulin homology <IM3>
F;296-347/Domain: immunoglobulin homology <IM4>
F;296-347/Domain: immunoglobulin homology <IM4>
F;372-395/Domain: transmembrane #status predicted <IM7>
F;372-395/Domain: intracellular #status predicted <IM7>
F;396-432/Domain: intracellular #status predicted <IM7>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: C32722
R; Camerini, D.; Seed, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell surface N; Alternate nam
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A; Residues: 1-432 < CAM>
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A; Accession: C32722
  Query Match
Best Local S
Matches 146
                                                                                                             Introns: 99/1, 112/1; 219/1
;Introns: 99/1, 112/1; 219/1
;Superfamily: immunoglobulin C region; immunoglobulin homology;
;Keywords: glycoprotein; immunoglobulin; membrane protein
;Reywords: glycoprotein; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 152; Conserv
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                                                                                                 /Binding site:
                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSSPSVKCRSPGGKNIQGGRTISVPQLERQDSGTWTCTVSQDQKTVEFKIDIV
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     Conservative
                                                                                                 carbohydrate (Asn)
                         28.6%;
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; Pred. No. 9.4e-40;
12; Mismatches 10
                         Score 774; DB 2; Pred. No. 6e-39;
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     Mismatches
                                                                                              (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-180 <HEI>
A;Cross-references: GB:J00665; NID:g165109; PIDN:AAA31288.1; PID:g165110
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;93-160/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                              R;Heidmann, O.; Rougeon, F.
Nucleic Acids Res. 10, 1535-1545, 1982
A;Title: Molecular cloning of rabbit gamma
A;Reference number: I46732; MUID:82174328;
A;Accession: I46732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma heavy chain constant region - rabbit (fragment) c;Species: Oryctclagus cuniculus (domestic rabbit) C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text C;Accession: I46732
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Matches 124; Conser
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                    NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                      EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
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DNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPG
                                                                            PAPIEKTISKARGOPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAE
                                                                                                                                                       DDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                    26.0%;
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                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                      Score 702; DB 2; Pred. No. 5.6e-35;
                                                                                                                                                                                                                                    Mismatches
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PMID:6280149
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CD4 precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994

#text\_change

21-Jan-2000

Recker, λq

D.P.; human

Kindt,

T.J.

immunodeficiency

**S**.

A46254

A;Cross-references: GB:M92840; NID:g164871; PIDN:AAA31198.1; A;Note: sequence extracted from NCBI backbone (NCBIN:112732, C;Superfamily: T-cell surface glycoprotein CD4; immunoglobuli

PID: 9164872 NCBIP: 112733)

surface glycoprotein

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-459 <HAG>

A; Reference number: A46254; A; Accession: A46254

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RBSULT 43
330193
T-cell surface glycoprotein CD4 - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S30193
R;Milde, K.F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
Biochim. Biophys. Acta 1172, 315-318, 1993
A;Title: Primary structure of the canine CD4 antigen.
A;Reference number: S30193; MUID:93192324; PMID:7916632
A;Accession: S30193;
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A; Residues: 1-432 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;322-372/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153;
                           183 TCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTP
                                                                           120 GSSSGSSNIRLLOGOOLILILENPSGSSPSVOWKGPGNKSKHGGONLSLSWPELODGGTW 179
                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
180
                                                                                                                                                                                                                                                                                                                              tch 21.5%; al Similarity 32.8%; 170; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 -LDKG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CLVKG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 SAQSWVSFSLEDRKVSVQKILP---DLKIQMSKGLPLS---LTLPQALHRYAGSGNLSLT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 QDSGTWTCTV-LQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 LMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                          12 LVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                              1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 22.3%; Score 601.5; DB 2;
Similarity 41.9%; Pred. No. 1.6e-28;
53; Conservative 47; Mismatches 98;
                                                                                                     -----NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW 182
                                                                                                                                                             GSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS 119
                                                                                                                                                                                    GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGNQG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNRRIYFQCLLLVLPLALLPAATWGKTVVRGKAGAIVELPCQSSQKRNSVFNWKHANQVK 60
TCIISQSQKTVEFNINVLVLAF---QKVSNTFYARE--GDQVEFSFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDSGTWSCHLSFQDQNKLELDIKIIVLGFPKASA----TVYKKEGEQVEFSFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVELLVFRLTANPNTRLLHGQSLTLTLEGPSVGSPSVQWKSPENKIIETGPTCSMPKLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILGNOGSSSSSFWLKGNSPLSNRVESKKNMWDQGSFPLVIKDLRMDDSGTYICEVGDKKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LNFEDESLSGELMWQVDGAS---
                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                            Score 581.5; DB 2;
Pred. No. 2.3e-27;
7; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                                                                                                                Indels 129;
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221
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RESULT 45 S69340 Ig heavy chain VHII C;Species: Homo sap C;Date: 28-Oct-1996 C;Accession: S69340 R;Khamlichi, A.A.; Eur. J. Biochem. 22 A;Title: Structure: A;Reference number: A;Reference number: A;Recession: S69340 A;Status: prelimina: A;Molecule type: mRIA;Residues: 1-249 <: A;Cross-references:	Qy 4	94 84 84	\$ &	Query Match Best Local Matches 11	A;Status: I A;Molecule A;Residues: C;Superfami C;Keywords: F;132-199/I	R;Eulitz, R Proc. Natl. A;Title: In A;Reference A;Accession	RESULT 44 A36040 Ig heavy ch C;Species: C;Date: 16- C:Accession	Qy VQ	Qy db	Db Qy		<b>₽</b>	QV .
RESULT 45 S69340 C;Species: Homo sapiens (man) C;Species: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000 C;Accession: S69340 C;Accession: 569340 Eur. J. Biochem. 229, 54-60, 1995 A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687; PMID:7744049 A;Status: preliminary A;Molecula type: mRNA A;Residues: 1-249 <kha> A;Cross-references: EMBL:X81696</kha>	410 CSVMHEALHNHYTQKSLSLSPG 431 .                     197 CSVMHEGLHNHYTQKSLSLSPG 218	350 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 409 	290 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 349	ch 21.3%; Score 574.5; DB 2; Length 218; al Similarity 77.5%; Pred. No. 2.6e-27; 110; Conservative 3; Mismatches 12; Indels 17; Gaps 1;	A;Status: preliminary A;Molecule type: protein A;Molecule type: protein A;Residues: 1-218 <eul> C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;132-199/Domain: immunoglobulin homology <ivm></ivm></eul>	4.; Welss, D.T.; Solomon, A. Acad. Sci. U.S.A. 87, 6542-6546, 1990 munoglobulin heavy-chain-associated amyloidosis. number: A36040; MUID:90370821; PMID:2118650	nain V-III region (ART) - human (fragments) Homo sapiens (man) Nov-1990 #sequence_revision 16-Nov-1990 #text_change 21-Jan-2000	476 SALPDPPAASALPAALAVISFLLGLGLGVAC 506	419 NHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTA 475	359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418 	49 FTLENRKLSMKEAHAPLKLQMKESLPLRFTLPQVLSRYAGSGILTLNLAKGTL 30	222SPEDENIVGELRWQAQGASSSLLWIS 248	243 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 300

C; Superfamily: immunoglobulin C region; immunoglobulin homology

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RESULT 47

A27449

A27449

T-cell surface glycoprotein CD4 precursor - rat

T-cell surface glycoprotein CD4 precursor - rat

T-cell surface glycoprotein CD4 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A27449; A3543

R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987

A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: eviden A;Reference number: A27449; MUID:87175535; PMID:3104900

A;Accession: A27449; MUID:87175535; PMID:3104900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Construction and characterization of a recombinant murine monoclonal A;Reference number: S14236; MUID:91006173; PMID:2209622 A;Accession: S14236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, Eur. J. Biochem. 192, 767-775, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma-1 chain C region (15C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                      A; Molecule type: mRNA
A; Residues: 1-457 < CLA>
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A; Residues: 1-152 < VAN>
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Best Local
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8-references: GB:M15768; NID:g203387; PIDN:AAA40901.1; PID:g203388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%; Score 566; DB 2; 61.6%; Pred. No. 5.4e-27;
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Pred. No. 4e-
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R;Davis, S.J.; Ward, H.A.; Puklavec, M.J.; Willis, A.C.; J. Biol. Chem. 265, 10410-10418, 1990
A;Title: High level expression in Chinese hamster ovary c A;Reference number: A35433; MUID:90285164; PMID:2113054
A;Contents: annotation
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Best Local (
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                                  GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 413
                                                                     QSWITFSLKNQKVS-----VQKSTSNPKFQLSE----TLP---
                                                                                                     QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355
                                                                                                                                                                                                             DSGIWNCTVTLNQKKHSFDMKLSVL-----GFASTSITAYKSEGESAEFSFP-----
                                                                                                                                                                                                                                            DSGTWTCTVLQNQKKVEF--KIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
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                                                                                                                                                                                                                                                                                                                 QLIVEGLTANSDIHLIQGOSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLEIQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                          MCRGFSFRHLLPLLLLQLSKLLVVTQGKTVVLGKEGGSAELPCESTSRRSASFAWKSSDQ
----PQVSLQFAGSG----NLTLT---LDR-GILYQEVNLVVMKVTQPDSNTLTCEVM
                                                                                                                                          -----KAEKAPSS----
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No. 3.3e-22;
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7; Mismatches
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RWMST4

Science 234, 610-614, 1986
A;Title: Isolation and sequence of L3T4 complementary DNA clones: expression A;Reference number: A02110; MUID:87018845; PMID:3094146 C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Jul-1999 C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642 R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. T-cell surface glycoprotein CD4 precursor - mouse N; Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen A; Accession: A02110 C; Species: Mus musculus (house mouse) ä T4/Leu н cells

A; Molecule type: mRNA A; Residues: 1-457 < TOU>

Nature 325, 453-455, 1987 A; Title: Unusual intron in A;Cross-references: GB:M13816; NID:g192070; PIDN:AAA37267.1; R;Littman, D.R.; Gettner, S.N. A; Reference number: A26038; ;Littman, D.R.; Gettner, in the immunoglobulin domain of 038; MUID:87115821; PMID:3027575 the newly isolated PID:g309112

murine

g

F

A; Accession: A26038

PID:g50354

in brain

A;Molecule type: mRNA
A;Residues: 1-457 <LIT>
A;Residues: 1-457 <LIT>
A;Residues: 1-457 <LIT>
A;Cross-references: GB:X04836; NID:g50353; PIDN:CAA28539.1;
A;Corman, S.D.; Tourvieille, B.; Parnes, J.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
A;Title: Structure of the mouse gene encoding CD4 and an unu
A;Reference number: A39893; MUID:88041159; PMID:2823269
A;Accession: A39893 unusual transcript

A; Molecule type: DNA A; Residues: 1-25, 'E', 27-457 < GOR>

A;Cross-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID: 9387124

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Ig Y heavy chain (7.8S) - duck
N;Alternate names: Ig gamma chain (7.8S)
C;Species: Anas platyrhynchos (domestic
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(;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: alternative initiators duplication; glycoprotein; T-cell; trans
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;35-114/Domain: immunoglobulin homology <IM1>
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A; Residues: 208-318 <RE2>
A; Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1;
A; Classon, B.J.; Tsagaratos, J.; Kirszbaum, L.; Maddox, J.; KIRSIDAUM, L.; Maddox, J.; M.
Immunogenetics 23, 129-132, 1986
A; Title: The L3T4 antigen in mouse and the sheep equivalent a A; Reference number: A47642; MUID:86166694; PMID:3082751
A; Accession: A47642
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A;Title: L3T4 and the immunoglobulin gene superfamily: New relationships between
A:Reference number: I54564; MUID:88152875; PMID:3326818
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A;Title: Structure and expression of the human and mouse T4 genes.
A;Reference number: A39955; MUID:88097446; PMID:3501122
A;Accession: A39955
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A;Residues: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of mature
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A; Residues: 1-457 < RES>
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A;Residues: 25-457 <MAD>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCRAISLRRLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILGQHGKGVLIRGGSPSQF-DRFDSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILGNQG-SFLTKG--PSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
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52.8%;
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Pred. No. 5.1e-21
2; Mismatches 5
             duck)
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Mackay, C.R.
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Ig heavy chain precursor - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C;Accession: S04845; 805695
R;Amemiya, C.T.; Haire, R.N.; Litman, G.W.
Nucleic Acids Res. 17, 5388, 1989
A;Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin A;Reference number: S04845; MUID:89345103; PMID:2503814
A;Accession: S04845
                                              A;Molecule type: mRNA
A;Residues: 'LC',3-308,'H',310-549 <LIT>
A;Residues: 'LC',3-308,'H',310-549 <LIT>
A;Cross-references: EMBL:X15114; NID:964799; PID:9763031
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterocetramer; immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
F;26-109/Domain: immunoglobulin homology <IMM>
F;281,294/Binding site: carbohydrate (Asn) (covalent) #status p
                                                                                                                                                                                                                                             submitted to the EMBL Data Library, April 1989 A;Reference number: S05695
                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-549 <AME>
A;Cross-references: EMBL:X15114
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                                                                                                                                                                                                                                                                                                   R;Litman,
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A; Residues: 1-572 < MAG>
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R;Magor, K.E.; Warr, G.W.; Middleton, D.;
J. Immunol. 149, 2627-2633, 1992
                                                                                                                                                                                                                         A;Accession: S05695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X65219; NID: g62442; PIDN: CAA46322.1;
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  Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGKNIQGGKTLSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFLYSKMTVPKASWQGGVSYACMVVHEGLPMRFTQRPLQKTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW--ESNGQPENNYKTTPPVLD--SDGS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPMVLTEHFNGTFTASSSLAISTQDWLAGERFTCTVQHEDLPVPLGKSIAKHAGKVTAPY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSKTYMATSQTNVSREDWKAGKAFTCRVKHPATGGTAQGHARF-----CPGSGAQSCSP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDSVELLCVITGFSPPPVEVEWLVDGAPAH------LVATMTRPQ------REA 306
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  Score 402.5;
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                                              (Asn) (covalent) #status predicted
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  Length 549;
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A;Molecule type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-627/Product: Ig mu chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change C;Accession: $14683; $08047
C;Accession: $14683; $08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of th A;Reference number: $14683; MUID:90332450; PMID:2115996
A;Accession: $14683
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C;Species: Homo sapiens (man)
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  THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                                                             LELODSG-----
                                                                                                                                                               AELPPKVSVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQ
                                                                                                                                                                                                                        LESPPGSSPSVQCR------
                                                                                                                                                                                                                                                                       SVLRGGKYAATSQVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                             LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                               SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------
                                                                                                                                                                                                                                                                                                                                                                                                                                  TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEGFISFSKLTIARSDWMRGATYSCI----AAHNTISQRDIKKNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSFFL-YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEPTITLLPPSDDELRNDFISLICMLKNFRPQDIYVFWKKDGVTLEEDYYMTTTPVLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG--QPENNYKTTPPVLDSD 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALAFDSAP-EKAYDGTFTVKSTLKISPGDWENKKQFNCKVVHPDLPSPIEKSIQKSQDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EASTKKCDETAITPKVDVLPPSPKD-LLVTKEAKVYCVISRMASTD-DLTVQWSRSDGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DOKEEVQ---LLVFGLTANSDT-------HLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGSITSGLKNFPAVLQQSGLFASSSQLTIPLSDWKAKKSFECNVEHKPTSTKVTQKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDQG-----NFPLIIK------NLKIEDSD----TYICEVE------
                                                     AEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KP---CKEENG-TFSSRSKVSVPKEDWNSEDSYTCKVTH-----PASHTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.1%; Pred. No. 1.3e-16; tive 65; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 389; DB 2; Length 627;
23.9%; Pred. No. 9.6e-16;
Live 77; Mismatches 167; Indels 1
                                                                                                          -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                  SPR-----GKNIQGGKTLSVSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-388 <-LIU>
A;Cross-references: GB.J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
A;Cross-references: GB.J00476; NiD:g194875; PIDN:AAA38085.1; PID:g387220
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-44/Domain: immunoglobulin homology (fragment) <IM1>
F;186-254/Domain: immunoglobulin homology <IM3>
F;186-254/Domain: immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA
A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Accession: A02144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig epsilon chain C region (version 1) C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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376 YKTTPPVLDSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG
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                                                     VRSITKTPGQRSAPEVYVFPPPEEE-SEDKRTLTCL1QNFFPEDISVQWLGDGKL1SNSQ
                                                                                                                                                                                                                                                                                                                                                                               AQTVLIKE-EGKLASTCSKLNITEQQWMSESTFTCKV--TSQGVDYLAHTRRCPDHEPR-
                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKS
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                                                                                                       EKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENN--
                                                                                                                                                                                                                                                                                                                          CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVNITEPTLELLHSSCDPNAFHSTIQLYCFIYGHILNDVSVSWLMDDREITDTL-----
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                                                                                                                                                                                                               WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
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                                                                                                                                                               -----NATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPI
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Pred. No. 6.2e-16;
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A;Title: mRNA transcripts initiating within the human immunoglobulin mu A;Reference number: S15590; MUID:91252286; PMID:1904154 A;Accession: S15590
      Mo.1
                Ig mu chain C region - human C;Species: Homo sapiens (man) C;Date: 12-Feb-1998 #sequence C;Accession: S37768 R;Harindranath, N.; Donadel,
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A;Molecule type: mRNA
A;Residues: 1-474 <NEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X58529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: immunoglobulin C region; imm; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
   30,
                                                                                                                                                                                              GLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------
                                                                                                                                                                  NLWAT
                                                                                                                                                                                                                                                          SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
                                                                                                                                                                                                                            RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS
                                                                                                                                                                                                                                                                                                                                                                                    TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYLLPPAREQUILRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG 390
                                                                                                                                                                                                                                                                                                                       VYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                        TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELQDSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVAVGCLAODFLPDSITFSWKYKNNSDISSTRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
.; Donadel, G.;
111-112, 1993
                                                                                                                                                                                              452
                                                #sequence_revision 12-Feb-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                    --VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGQAVKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; SCUL. 9.7e-1.
23.7%; Pred. No. 9.7e-1.
rtive 78; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the codon CAA for residue 265 as Glu
C region; immunoglobulin homology
                  Sigounas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
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F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-88,134-197,244-303,351-413/Disulfide bonds: #status predicted
F;26-88,134-197,244-303,351-413/Disulfide bonds: (Asn) (covalent) #status
F;46,209,272,279,440/Binding site: carbohydrate (Asn) (covalent) #status
F;214,452/Disulfide bonds: interchain (to heavy chain) #status predicted
F;291/Disulfide bonds: interchain (to mu chain in another subunit) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-453 <HAR>
A;Cross-references: EMBL:X67301; NID:g38407; PIDN:CAA47714.1; PID:g38408
A;Experimental source: cell line Ab 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;291/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: glycoprotein; heterotetramer; immu;21-90/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: immunoglobulin C region; immunoglobulin homology; Superfamily: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                          LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                          REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI
                                                                                                                                     RDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSK
                                                                                                                                                                                  PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                                                                                                                             YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                                                                                                                                                                                                                                          ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                                   GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                     TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSVQCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
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3; Mismatches
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Pred. No. 1.1e-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SPR-----GKNIQGGKTLSVSQLELQDSG-
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                                             431
434
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S25705

Ig mu chain - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999
C;Accession: S25705
R;Patri, S.; Nau, F.

Mol. Immunol. 29, 829-836, 1992
A;Title: Isolation and sequence of a cDNA coding for the immunoglobulin mu
A;Reference number: S25705, MUID:92342148; PMID:1635560
A;Accession: S25705
A;Accession: S25705
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-592 cPAT>
A;Cross-references: EMBL:X59994; NID:g1269; PIDN:CAA42611.1; PID:g1270

chain

e F

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A; Molecule type: DNA
A; Residues: 433-473 40R1>
A; Cross-references: EMBL:X14939
A; Note: the authors translated the codon AAC for residue
A; Note: the sequence of residues 1-432 was assumed to be
A; Accession: S09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 29-Jan-1993 #sequence revision 23-Aug-1997 #text_change 22-Jun-1999 C;Accession: S16510; S09357; Š16656; B26243; A02167 R;Doral, H.; Gillies, S.D.
Nucleic Acide Res. 17, 6412, 1989
A;Title: The complete nucleotide sequence of a human immunoglobulin genomic C-mu A;Reference number: S09357; MUID:89366690; PMID:2505237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
MHHUM
  R;Rabbitts, T.H.; Forster, A.; Milstein, C.P. Nucleic Acids Res. 9, 4509-4524, 1981 A;Title: Human immunoglobulin heavy chain gen
                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: S16656
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                                                                         A; Molecule type: DNA
A; Residues: 1-39, L', 41-432, GKPTLYNVSLVMSDTAGTCY'
                                                                                                                           A; Reference number: A; Accession: S16656
                                                                                                                                                                                         R; Dorai,
                                                                                                                                                                                                                            A;Cross-references: EMBL:X14940 A;Note: the authors translated the
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-432, 'GKPTLYNVSLVMSDTAGTCY'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig mu chain C region, membrane-bound C; Species: Homo sapiens (man)
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                                                              A; Cross-references: EMBL: X14940
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Best Local S
Matches 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG-QPREPQVYTLPPSR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYSVLTITEREWLSQSAYTCQVEHNKETFQKNAS-----SSCDATPPSP--IG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDTFSARGEASVCSEDWESGEEYTCTVAHLDLPFPEKSAISKPKDVAMKPPSVYVLPPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFTIPPSFAD-IFLTKSAKLSCLVTNLASYD-GLNISWSHQNGKALETHTY----FERHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW-YVDG--VEVHNAKTKPREEQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSLTLTLESPPGSSPSVQCR----SPR-----GKNI-----QGGKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVTEEDWSKGETYTCVVGHEALPHMVTERTVDKSTG 573
immunoglobulin heavy chain genes:
                                                                                                                                                                                                             splice form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 384; DB 2;
Pred. No. 1.8e-15;
                                                                                                                                                                                                                              codon AAT for
                                                                                                                                                                  April . 1989
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evolutionary comparisons
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of C-mu,
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C-del
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RESULT
S38864
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A;Introns: 1/1; 105/1; 217/1; 323/1; 433/1; 471/3
C;Complex: An immunoglobulin heterotetramer subunit consists of hain disulfide bonds. The IgM subunits associate into disulfide C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; glycoprotein; heterotetramer; F;21-90/Domain: immunoglobulin homology <IMM1>
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A;Accession: B26243
A;Accession: Lype: DNA
A;Molecule type: DNA
A;Residues: 433-436,'N',438,'E',440-447,'T',449-473 <RAB>
A;Cross-references: GB:K01310; NID:g184715; PIDN:AAB59422.1;
C;Comment: During differentiation, B lymphocytes switch from
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Best Local S
Matches 116
                  57
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                                                                            NEWAT
                                                                                                                   GLWTT 452
                                                                                                                                                           RYFAHSILTVSEEEWNTGETYTC-VAHEALPNRVTERTVDKS----
                                                                                                                                                                                                                                                                                                                                        TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-
                                                                                                                                                                                            SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
                                                                                                                                                                                                                                                                        VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                     HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAKESGPTTYKVTSTLTIKESDWLGQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESPPGSSPSVQCR-----
                                                                                                                                                                                                                                     VYLLPPAREQUNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                                                    TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 381; DB 1; Length 473; 23.9%; Pred. No. 2.1e-15; vative 77; Mismatches 166; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 126;
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expression
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Ig epsilon chain C region - mouse (frag C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence\_revision

- mouse (fragment)

06-Jan-1995

#text\_change 24-May-2001

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A; Decause gran
A;Molecule type: mRNA
A;Residues: 1-190,'S',192-414,'V',415-452 <HAR>
A;Residues: 1-190,'S',192-414,'V',415-452 <HAR>
A;Crona-references: EMBL:X67292; NID:g38405; PIDN:CAA47708.1;
                                                                                                                      A; Molecule type: DNA
A; Residues: 1-39, 'L', 41-452 < DOR2>
A; Cross-references: EMBL:X14940
R; Harindranath, N.; Donadel, G.; Sigounas, Mol. Immunol. 30, 111-112, 1993
A; Title: Comparison of complete nucleotide
A; Reference number: S37767; MUID:93109369;
A; A; Accession: S37767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo Bapiens (man)
C;Date: 29-Jul-1981 #sequence revision 23-Aug-1997 #text change 22-Jun-1999
C;Accession: S09357; S16656; S37767; A26243; A26244; I37749; I37750; A02162;
R;Doral, H; Gillies, S.D.
Nucleic Acids Res. 17, 6412, 1989
A;Title: The complete nucleotide sequence of a human immunoglobulin genomic C
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                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A;Reference number: S16656
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A;Description: Combination of a defined specificity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S38864
R; Kipp, B.; Becker,
                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         R;Dorai,
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X14940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S09357; A; Accession: S09357
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                                                                                                                                                                                                                                                                                                                                                                                           A; Note: the authors translated the codon AAT for
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-452 < DOR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLEVAKTLWTORKOFTCOVIHEALOKPRKLEKTISTS 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLS 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEEE-SEDKRTLTCLIQNFFPEDISVQWLGDGKLISNSQHSTTTP-LKSNGSNRGFFIFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTEQQWMSESTFTCKV--TSQGVDYLAHTRRCPDHEPR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSTIQLYCFIYGHILNDVSVSWLMDDREITDTL-----AQTVLIKE-EGKLASTCSKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEEVQL--LVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otide sequence of
MUID:89366690; אַס
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 381; DB 2;
Pred. No. 2.4e-15;
                                                                                                                                                                                                                                                                                                                                                  April 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 106; Indels
                                                                                                                                               sequence of the human PMID:8417370
                                                                                                                                                                                                              G.; Notkins, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a human immunoglobulin genomic C-mu
PMID:2505237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                residue
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                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                98
                                  PID: 938406
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                                                                                                                                                                    Igm heavy chain
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A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 1493:33-1493:33
A;Introns: 1/1; 105/1; 237/1; 333/1; 433/1
C;Complex: An immunoglobulin heterotetramer subunit consists of hain disulfide bonds. The IgM subunits associate into disulfide C;Superfamily: immunoglobulin C region; immunoglobulin homology c;Keywords: alternative splicing; glycoprotein; heterotetramer; F;21-90/Domain: immunoglobulin homology cIMM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Molecule type: protein
A;Residues: 100-144, 'E',146-162, 'E',164, 'E',166-214, 'G',216-262, 'D',264-295, 'D',297-414,
A;Residues: 11 four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms have been
A;Note: all four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms have been
A;Natanabe, S.; Barnikol, H.U.; Horn, J.; Bertram, J.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1505-1509, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I
                                                          F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;342-452/Domain: carboxyl-terminal <CTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete amino acid sequence of the mu heavy chain of a human IgM immunoglobulir A;Reference number: A02088; MUID:74005511; PMID:4742735 A;Contentes: annotation; Waldenstrom's macroglobulin Ou, sequence, disulfide bonds, and ca A;Note: this sequence differs from that shown at a number of positions; this sequence has C;Comment: During differentiation, B lymphocytes switch from expression of membrane-bounce.
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A;Residues: 1-17;105-186;200-259;296-322;339-416,'D',418-452
A;Cross-references: GB:K01310; NID:g184715
A;Cross-references: GB:K01310; NID:g184715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: this sequence has R; Putnam, F.W.; Florent, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-17,'BPS',22,'T',24-82,'N',84-90,'Z',92-93,'B',95,'B',97-144,'E',146-162,'E
A;Accession: B02162
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A;Title: Cloning of human immunoglobulin mu gene and comparison
A;Reference number: 137748; MUID:81124312; PMID:6450943
A;Accession: 137749
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Nucleic Acids Res. 8, 5983-5991,
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Proc. Natl. Acad. Sci. U.S.A. 77, 6027-6031, 1980
A;Title: Cloning and partial nucleotide sequence of human immunoglobulin mu
A;Reference number: A26244; MUID:81077306; PMID:6777778
                                      F;14/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: IGHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 182, 287-291, 1973
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R;Mihaesco, E.; Barnikol-Watanabe, S.; Barnikol, H.U.; Mihaesco, C.; Hils
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A; Residues: 433-452 < TAK2>
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R;Takahashi, N.; Nakai, S.; Honjo, T.
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A; Residues: 298-386; 436-452 < DOL>
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;14/Disulfide bonds: interchain (to light chain) #status;28-88,134-197,244-303,351-413/Disulfide bonds: #status 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A02162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation; Waldenstrom's macroglobulin Gal
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Shinoda, T.; Shimizu,
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experimental experimental
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                                                                                                                                                                                                                                                                                                                                      two identical light linked pentamers.
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Nucleic Acids Res. 17, 1776, 1989

A;Title: A second Xenopus immunoglobulin heavy chain constant A;Reference number: S03186
A;Accession: S03186
A;Accession: S03186
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A; Residues: 1-448 < HAI>
A; Cross-references: EMBL: X13779; NID: 964827; PID: 964828
A; Cross-references: EMBL: X13779; NID: 964827; PID: 964828
A; Note: the authors translated the codon TTT for residue 9 as Ser C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: S0316
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVLRGGKYAATSQVLLPSKD-------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
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                                                                                           KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP----
                                                                                                                             ADPLDIQWNDGSITTGIKTMRPVLSDVDGLYTLSSQLTILASEWKNSTYKCKVVHNYTNT
                                                                                                                                                                 ADSRRSLWDQGNFPLIKNLK--IEDSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYFAHSILTVSEEEWNTGETYTC-VAHEALPNRVTERTVDKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
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                                                          KQEKSLKVLPCMA--
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24.1%;
                                                                                                                                                                                                  13.8%; Score 374; DB 2; 1
26.8%; Pred. No. 5e-15;
Live 57; Mismatches 144;
-SVQCRSPRGKNIQGGKTLSVSQLELQDSGTW-----TCTVLQN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75; Mismatches 156;
                                                        ---PHVQLFLQSPCMSDAISRAQHENINATLDLLCIINNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 376.5; DB 1;
Pred. No. 3.6e-15;
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421
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                                                                                                                                                                                   GDKFSCTVRSQDLPSPVKXTIFKQNEGTPKAPDVYLLPPSAQELIQQEMVTLTCFVTGFN
ALPLYITQQSIDKSSG
                                            ALHNHYTOKSLSLSPG
                                                                                            PKEIFIQWMQGGVSISEDKFINTVPMKSDGEQTYFIYSKLAIPAAKWNQGDVFTCVVGHE
                                                                                                                          PSDIAVEWESNG---QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHB
                                                                                                                                                                                                                                     GKEYKCKVSNKALPAPIEKTISKA-KGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFY
                                                                                                                                                                                                                                                                                       SMKTIENFDISWEREKAGNLEFVTEDPVLHD-----NGTYSVASILSVCAEDWES
                                                                                                                                                                                                                                                                                                                                      ----VDVSHEDPEV-KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
                                                                                                                                                                                                                                                                                                                                                                                                                                   QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV-
436
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Ig mu chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Oct-1980 #sequence revision 30-Jun-1991 #text\_change 22-Jun-1999 C;Accession: A02167; A37517; B02166 A;Title: Two mRNAs can be produced from a single immunoglobulin A;Reference number: A02167; MUID:80222874; PMID:6771020 A;Accession: A02167 R; Early, P.; Rogers, J Cell 20, 313-319, 1980 60 J.; Davis, M.; Calame, K.; Bond, M.; Wall, 킖 R.; Hood, gene by alternative

A; Residues: 436-476 < EAR > A; Molecule type: DNA

A;Cross-references: GB:V00816; GB:J00444; NID:g52343; R;Rogers, J.; Early, P.; Carter, C.; Calame, K.; Bond, Cell 20, 303-312, 1980 PIDN:CAA24197.1; PID: , M.; Hood, L.; Wall, :952344 R.

A;Title: Two mRNAs with different 3' ends encode membrane-bound A;Reference number: A37517; MUID:80222873; PMID:6771019 A;Contents: MOPC 104E and secreted forms Ğ.

A; Accession: A37517

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 410-476 < COG>
A; Cross-references: GB: V00821; NID: g52355; PIDN: CAA24202.1; PID: g817972
A; Cross-references: GB: V00821; No.; Honjo, T.
A; Kawakami, T.; Takahashi, N.; Honjo, T.
Nucleic Acids Res. 8, 3933-3945, 1980
A; Title: Complete nucleotide sequence of mouse immunoglobulin mu gene and comparison wit A; Reference number: A02166; MUID: 81076590; PMID: 8255422
A; Reference number: A02166; MUID: 81076590; PMID: 8255422
A; Molecule type: DNA
A; Residues: 1-435, GKPTLYNVSLIMSDTGGTCY' < KAW>
C; Comment: The sequence of residues 1-409 was assumed to be identical with the corresponcy; C; Comment: During differentiation, B lymphocytes switch from expression of membrane-bounce.

8.

G;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kathain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1-C;Superfamily: Immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; f;21-91/Domain; immunoglobulin homology <IMM1>

F;129-20/Domain: immunoglobulin homology <IMM2>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: immunoglobulin homology <IMM4>
F;436-476/Domain: immunoglobulin homology <IMM4>
F;436-476/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted F;28-89,136-199,246-305,353-415/Disulfide bonds: #status predicted F;46,211,243,258,281/Binding site: carbohydrate (Asn) (covalent) #status predicted F;216/Disulfide bonds: interchain (to heavy chain) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted predicted

Query Match Best Local Similarity 13.8%; 25.2%; Score 373.5; DB 1; Pred. No. 5.8e-15; Length 476;

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Ig epsilon chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
C;Date: 17-Dec-1987 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin
A;Reference number: A93442; MUID:83064537; PMID:6292865
                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 'N', 169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;19-80/Domain: immunoglobulin homology <IMI>
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                                                                                                                                                                                                                                                                                                                                              A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: A;Reference number: A90937; MUID:83182019; PMID:6820340
A;Contents myeloma IR162
A;Accession: A90937
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain LOU/c/Wsl, immunocytoma IR; R;Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., DNA 1, 335-343, 1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A93442
                                                                                                                                                                                             ;118-186/Domain:
                                                                                                                                                     :118-186/Domain: immunoglobulin homology <IM2>;223-291/Domain: immunoglobulin homology <IM3>;327-398/Domain: immunoglobulin homology <IM4>
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                                                                                                                                   ,170,240,265,369,419/Binding site: carbohydrate
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               160 GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
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                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAREQUALRESATVICLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGO--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPP----GSSP---SVQCR----SPR-----GKNIQGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                         Conservative
13.7%; Score 370.5; DB 1; 31.5%; Pred. No. 7.7e-15; ative 62; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                       homology <IM2>
homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TEGEVNAEEEGFENLWTT
                                                         Indels
                                                                                                                                   (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              C.H.
                                                                                                                                   (covalent) #status predicte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A02165
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                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                     148
                                                                                                                                                                                                                                                                                                                                              123;
188
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                                                                           -----GKNIQGG-
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                              13.7%;
                                                                                                                                                                                                                                                                                                                                              79;
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F;130-202/Domain: immunoglobulin homology <IMM2>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted F;28-99,137-200,249-308,356-418/Disulfide bonds: #status predicted F;46,114,212,261,277,284/Binding site: carbohydrate (Asm) (covalent) F;219/Disulfide bonds: interchain (to heavy chain) #status predicted F;296/Disulfide bonds: interchain (to mu chain in another subunit) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the sequence of residues 1-438 was assumed to be identical with the correspondin C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases to the land IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;21_92/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-438, 'GKPTLYNVSLIMSDTASTCY' <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Complete sequence of a cloned cDNA encoding rabbit A; Reference number: A02164; MUID:84088930; PMID:6418803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, J. Immunol. 132, 490-495, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Oryctolagus cuniculus (domestic rabbit); Date: 04-Dec-1986 #sequence_revision 30-Jun-1991; Accession: A02165; A02164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mu chain C region, membrane-bound form -
QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                     SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                                                                                                                                                                                                                        VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                           NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
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                                                                                                                                                                                                                                                                                                                                                          ----SSRTV----RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
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                                                                                                                                                                                                                   -SFPVDSELPPNVSVFIPPRDSFSGSGTRKSRLICQATGFSPKQI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 369.5; DB
Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLARDFLPSSVTFSWSFKNNSEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 153;
                                                                                                                                              --KTLSVSQLELQDSGTW----TCTV----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology c[Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin place into la C;Superfamily: immunoglobulin homology <IMM1> F;20-199/Domain: immunoglobulin homology <IMM2> F;234-302/Domain: immunoglobulin homology <IMM3> F;341-412/Domain: immunoglobulin homology <IMM4> F;430-450/Domain: immunoglobulin homology <IMM4> F;440-450/Domain: immunoglobulin homology <IMM4> F;470-450/Domain: carboxyl-terminal <CTS> F;47/Disulfide bonds: interchain (to light chain) #status predicted prints bonds: interchain (to light chain) #status predicted prints predicted prints predicted prints predicted prints predicted prints predicted prints predicted predicted predicted predicted prints predicted predicted prints predicted predicted predicted prints predicted predicted prints predicted predicted prints predicted predicte
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A;Residues: 1-177 <MCC>
R;Wasserman, R.L.; Capra, J.D.
Science 200, 1159-1161, 1978
A;Title: Amino acid sequence of the Fc region of a canine immunoglobulin M: interspecies
A;Reference number: A94246; MUID:78180587; PMID:653360
A;Contents: Moo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; McCumber, L.J.; Capra, J.D.
Mol. Immunol. 16, 565-570, 1979
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C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jul-1981 #sequence revision 13-Jul-1981 #text_change 31-Mar-2000
C;Accession: A93131; A94246; A02169
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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       106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                      135 QGQSLTLTLESPPGSSPSVQCR------
                                                                                                                                            57
                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                         22 TVAMGCLARDFLPGSITFSWKYEBLSAINSTRG-----
                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                     LIIKNLK-----IEDSDTYI-CEVE----DQKEEVQLLVFGLTANSDTHLL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFDKNVSMSSECSTTPSP-------GIQVFPIAPSFADT-FLSKSARLICL
                                                                                                                                            SVLRGGKYVATSQVFLPSVDIIQGTDEHIVCKVRHSBGBKQKBVPLPVM------
                                                                                                                                                                                                                                                                                                                                                        TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHNHYTOKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVFVQWQQRGQPLSSDKYVTSAPAPEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFTCTVTHADLPFPLKHTISKSREVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTDLTTYG-SLNISW-----ASHNGKALDTHMNITESHPNATFSAMGEASVCAEDWESGE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPHMVTERTVDKS-----TEGEVGAEEEGFENLWTT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
LTL---PPEVSGFIPPRDAFFGBPRKSQLICQASGFSPRQVWSLRDGKQIESGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 369; DB 1; Length 450; 24.1%; Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  139;
                                                                      ----SPR-----GKNIQGGKT 168
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 156;
                                                                                                                                                                                                                                                                                         ----FP
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360	303 EYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPS	Ş
237	VTDLTTYD-SVT1SWTRQDGEAVKTHTN1SESHPNATFSAVGEASICEDDWD	g B
302	VVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK	Ś
178	_	B
242	190 -QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTP	Ś
128	9 KLICQATGFSPRQIEVSWLREGKQVGSGVTTDEVEAEAKESGPTTYKV	뮍
189	157SPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN	Ş
68	18 EAEDRIIKEEEARLSGRDMQVTSQPVIAELPPKVSVFVPPRDGFFGNPRKS	g
156	SVQLLVFGLTANSDTHL	Ś
15;	Query Match 13.5%; Score 365.5; DB 1; Length 391; Best Local Similarity 28.0%; Pred. No. 1.4e-14; Matches 105; Conservative .65; Mismatches 132; Indels 73; Gaps	3 M O
cted	3/Domain: immunoglobulin homology <imm2> 3/Domain: immunoglobulin homology <imm3> .0,217,378/Binding site: carbohydrate (Asn) (covalent) #status predi</imm3></imm2>	F;1
	3-391/Domain: Ig mu chain C region, secreted form <igm> 5-137/Domain: immunoglobulin homology <imm1></imm1></igm>	יניני יניני יניני
ransmembrane pro	mmunogrobulin nomology:terotetramer; immunoglobulin; t	100 100 100 100 100 100 100 100 100 100
	120086; OMIM:147020 -14q32.33	A A A
	,	≱;; 0;;
	Molecule type: protein Residues: 1-391 <bar> Comment: This protein has no V region homology or CH1 region.</bar>	Ω≱≱ ., , , ,
	os, MOID: OTIOTIOO,	A; A ?
chmann, N. amino-acid sequ	, S.; Mihaesco, E.; Mihaesco, C.; Barnikol, H.U.; Hils hysiol. Chem. 365, 105-118, 1984 y structure of mu-chain-disease protein BOT. Peculiar no:163. MITT.84184186. DMTT6425180	ъ нор В тор
	04-Dec-1986 #text_change 16-Ju	ი;, ი;,
	BSULT 64 HHUBT g mu heavy chain disease protein (Bot) - human ;Species: Homo sapiens (man)	RESULI MHHUBI Ig mu C;Spec
	435 LYNVSLVLSDTAGZ 448	D
	32LQLDETCAE	ફ
434	375 VTSAPMPEPQAPGLYFAHSILTVSEEEWNAGETYTCVVAHESLPNRVTERSVDKSTGKPT	В
431	377 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	Ş
374	315 ISRPKGVAVHMPSVYVLPPSREQLDLRESATLSCLVTGYSPPDVFVQMVQKGQPVPPDSY	<b>д</b>
376		ş
314	255 SWTREENGALKTHTNISESHPNGTFSAMGEATVCVEEWESGEQFTCTVTHTDLPSVLKQT	망
320		Ş
254	211 -CTSDQPVGISITTIPPS-FASIFNTKSAKLSCLVTDLATYD-SVTI	뫄
260	201 PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTÇVVVDVSHEDPEVKF	ş
210	: KVEHRGLTFQQNASSM	문
200	SGTVLQNQKKVEFKIDIV	S

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RESULT 65
EHMSS
                                                          RESULT 66
A24976
 Ig mu chain C region (allele b) - mouse C;Species: Mus musculus (house mouse) C;Date: 05-Jun-1988 #sequence_revision (
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F;220-288/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM4>
F;23-75,122-181,227-286,333-394/Disulfide bonds: #status
F;43,84,167,239,262,417/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin Cregion; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 1, 1117-1123, 1982

A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison A;Reference number: A90966; MUID:84236092; PMID:6329728
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A; Residues: 1-423 <ISH>
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A02145
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                                                                                                                                                                                                                                                                                                                                                                                                                                         162 TCSKLNITEQQWMSESTFTCRV--TSQGVDYLAHTRRCPDHEPR------GAI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 CEVEDQKEEVQL--LVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 13.5%; Score 363.5; DB 1; Length 423; Similarity 29.8%; Pred. No. 2e-14; O3; Conservative 68; Mismatches 114; Indels 61
                                                                                                                                                                      --FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG 431
                                                                                                                                                                                                                                 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN--YKTTPPVLDSDGS- 388
                                                                                                                                                                                                                                                                                                                                                             TYLIPPSPLD-LYQNGAPKLTCLVVDLESEKNVNVTWNQEKKTSVSASQWY---TKHHN-
                                                                                                                                 QGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDPNAFHSTIQLYCFIYGHILNDVSVSWLMDDREITDTL----AQTVLIKE-EGKLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPA
                                                                                                                                                                                                            EVYVFPPPEEE-SEDKRTLTCLIQNFFPEDISVQWLGDGKLISNSQHSTTTP-LKSNGSN 370
                                                                                                                                                                                                                                                                                    -----NATTSITSILPVVAKDWIEGYGYQCVVDRPDFPKPIVRSITLPQVSQRSAP 312
                                                                                                                                                                                                                                                                                                                      KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKÇKVSNKALPAPIEKTISKAK-GQPREP 331
                                                                                                                                                                                                                                                                                                                                                                                                    VFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN------WYVDGVEVHNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPNRVTERTVDKSTG
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#sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
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R;Schreier, P.H.; Qu
 A; Molecule type: DNA
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R;Schreier, P.H.; Quester, S.; Bothwell, A.

R;Schreier, P.H.; Quester, S.; Bothwell, A.

Rucleic Acids Res. 14, 2381-2389, 1986

A;Title: Allotypic differences in murine mu-genes.

A;Reference number: A24976; MUID:86176735; PMID:3083402

A;Accession: A24976

A;Molecule type: mRNA

A;Residues: 1-455 <SCH>
A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382

A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382

A;Experimental source: strain C57BL/6

A;Mote: the authors translated the codon AAG for residue 65 as Leu
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
A.Note: the sequence was determined from the germline gene R;Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R. Gene 15, 33-42, 1981
A;Title: Sequence of the gene for the constant region of the A;Reference number: A26239; MUID:82051295; PMID:8795090
A;Accession: A26239
                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence revision 31-Oct-1980 #text_change 16-Aug-1996
C;Accession: A02166; A26239; A26240; B02039
R;Kawakami, T: Takahashi, N: Honjo, T.
Nucleic Acids Res. 8, 3933-3945, 1980
A;Title: Complete nucleotide sequence of mouse immunoglobulin mu gene and coa; A;Reference number: A02166; MUID:81076590; PMID:6255422
A;Accession: A02166; MUID:81076590; PMID:6255422
                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-455 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig mu chain C region, secreted form
                                                                                                                                                                                                                            A;Cross-references: GB:J00443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAREQLNIRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST------DIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPP----GSSP---SVQCR----SPR-----GKNIQGG------
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A; Note: the seque
R; Auffray, C.; Ro
Gene 12, 77-86,
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A;Molecule type: mRNA
A;Residues: 1-225; 'N',227-257,'S',259-367,'K',369-455 < AUF>
A;Residues: 1-225; 'N',227-257,'S',259-367,'K',369-455 < AUF>
R;Rehry, M; Sibley, C.; Fuhrman, J.; Schilling, J.; Hood, L.E.
R;Rehry, Matl. Acad. Sci. U.S.A. 76, 2932-2936, 1979
A;Reference number: A26241; MUID:79223904; PMID:111247
A;Rontents: annotation; MOPC 104E
A;Rontents: annotation; MOPC 104E
A;Rote: this sequence has been revised in reference A02039. Carbohydrate binding sites
A;Rote: this sequence has been revised in reference A02039. Carbohydrate binding sites
R;Rehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain
A;Reference number: A02039; MUID:83075344; PMID:6816276
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455 <KEH>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                      PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                                                                                                      --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPP-----GSSP---SVOCR----SPR-----GKNIQGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT--
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PAREQUILLESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST------DIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 362; DB 1;
25.3%; Pred. No. 2.6e-14;
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A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog A;Reference number: A23195; MUID:84207910; PMID:6327276
A;Accession: A23195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; R;Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant A;Tetle: The sequence of a human immunoglobulin epsilon heavy chain constant A;Reference number: A22771; MUID:84236029; PMID:6234164
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Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon
A;Reference number: 136948; MUID:87147196; PMID:3103123
A;Accession: 136948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig epsilon-chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996
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A; Residues: 1-428 < FLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-426 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPREPQVYTL----PPSRDBLTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN--SDTHLLQGQSLTLTLESPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRAAPEVYAFATPEGPGSRDKRT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- DSTKKCADSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS
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Pred. No. 2.6e-14;
4; Mismatches 136;
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R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.

J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Grafin. A53116
A;Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167 A;Experimental source: B cell myeloma U-266 A;Note: sequence extracted from NCBI backbone (NCBIP:125297)
                                                                                                                                                                                   Eur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and a A;Reference number: A46536; MUID:93122085; PMID:8419166
A;Accession: C46536
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J. Exp. Med. 176, 233-243, 1992
A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing A;Reference number: PH1214; MUID:92308839; PMID:1613458
A;Accession: PH1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 224, 306-310, 1987
A; Title: Purification and characterization
A; Reference number: S02438; MUID:88083554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: myeloma protein Nd R; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human: A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: B93933
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A;Residues: 1-358,'L',360-428 <MAX>
A;Residues: 1-358,'L',360-428 <MAX>
A;Residues: GB.J00222; NID:g184755
A;Note: this sequence difference may be due to polymorphism
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments,
A;Reference number: A94418
A;Accession: A94418
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A;Title: Duplication and deletion in the human immunoglobulin epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 320-428 <ZHA-
A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
A;Cross-references: T.; Ono, Y.; Onda, H.; Sasada, R.;
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloning and nucleotide sequencing of
A;Reference number: A93491; MUID:83168897; PMID:6300763
A;Accession: A93491
                                                                                                 A; Molecule type: mRNA
A; Residues: 382-426 <HEL>
                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: myeloma U266-derived cell line AF-10 A;Note: sequence extracted from NCBI backbone (NCBIN:141701,
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A; Residues: 320-428 < ZH2>
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A;Residues: 1-40;68-114;427-428 <KEN>
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Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: mRNA
;Residues: 1-428 <SEN>
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;Zhang, K.; Saxon, A.; Max, E.E.
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                                                                                                                                                            compared with conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of a recombinant human IgE Fc-epsilon PMID:3121387
                                                                                                                                                            translation
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                                                                                                                                                                                                                                                                                                                                                      NCBIP:141702
                                                                                                                                                                                                                                                       comparative analysis
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A;Cross-references: GDB:11935; OMIM:147180
A;Cross-references: GDB:11935; OMIM:147180
A;Map position: 1432.33-14932.33
A;Mntrons: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap: nain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la: C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM1>
F;22-87/Domain: immunoglobulin homology <IM2>
F;232-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM4>
F;338-407/Domain: immunoglobulin homology <IM4>
F;338-407/Domain: immunoglobulin homology <IM4>
F;145-105.29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;11,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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A; Residues: 382-391 kHz>
A; Residues: 382-391 kHz>
A; Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1;
A; Experimental source: B cell myeloma U-266
A; Note: sequence extracted from NCBI backbone (NCBIP:125299)
A; Accession: A46536
C;Accession: $00390
R;Parvari, R; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.;
EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited
                                                                                                                                                                 Ig gamma chain (clone 36) - chicken N;Alternate names: Ig nu chain
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                                                                                                                                                                                                                        800390
                                                                                                                                                                                                                                                    RESULT
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                                                                                                 ;Alternate names: Ig nu chain
;Species: Gallus gallus (chicken)
;Date: 07-Sep-1990 #sequence_revision
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                                                                                                                                                                                                                                                                                                                               OPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPG
                                                                                                                                                                                                                                                                                                                                                                              PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRAAPEVYAFATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPREPQVYTL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DSTKKCADSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---STASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE----
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                                                                                                                                                                                          (fragment)
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                                                          Burstein,
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                                                       Y.; Schechter,
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A;Reference number: S00390; MUID:88283642; PMID:3135182 A;Accession: S00390

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gene

repertoire,

combinato H

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F;130-202/Domain: immunoglobulin homology <IRM2>
F;242-310/Domain: immunoglobulin homology <IRM2>
F;242-310/Domain: immunoglobulin homology <IRM3>
F;349-420/Domain: immunoglobulin homology <IRM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-90,137-200,249-308,356-419/Disulfide bonds: #status predicted
F;46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;419,457/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate int C;Superfamily: immunoglobulin cregion; immunoglobulin homology c;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;21-92/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete sequence of a cloned cDNA encoding rabbit A;Reference number: A02164; MUID:84088930; PMID:6418803 A;Contents: 82 allotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A02164
R;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J. Immunol. 132, 490-495, 1984
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A;Cross-references: EMBL:X07174
A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig mu chain C region, secreted form - rabbit
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
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             NDRADSRRSLWDQGNFPLIIKNLK--
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                                                                   ALTDGNLVAMG---
                                                                                                        AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPSPGE-LYISLDAKLRCLVVNLP-SDSSLSVTWTRE--KSGNLRPDPMVLQEHFNGTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNVSGTDWREGKSYSCRVRHPATNTVVEDHVKGCP-----DGAQSCSPI----QLYAI
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
<del>...</del>
                                                                                                                                                                      13.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 361; DB 2;
Pred. No. 3.4e-14;
                                                                                                                                                                   Score 360; DB 1;
Pred. No. 3.5e-14;
                                                                   CLARDFLPSSVTFSWSFKNNSEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                  Mismatches
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  -IEDSDTY-ICEVEDQKEEVQLL
                                                                                                                                                                                       Length 458;
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                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted
                                                                                                                                                  156;
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                                                                                                                                                                   RESULT 73
S03961
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Vopr. Virusol. 40, 100-102, 1995
A;Title: [Nucleotide sequence of two exons A;Reference number: I60082; MUID:95407135; A;Accession: I60082
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                                                                                                                                                                                      A; Introns: 17/1
C; Superfamily: 7
                                                                                                                                                                                                                                  A;Cross-references: GB:S79267; NID:g1086922; PIDN:AAB35273.1;
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-71 < RES>
                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                             C;Accession: I60082
R;Zverev, V.V.; Sidorov, A.V.; Nedospasov, S.A.; Maliushova, V.V.; Udalova, I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                              CD4 receptor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                             Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Homo sapiens (man)
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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                                                                                                                         70;
                                                                                                                                          Similarity
                ILGNQGSFLTK 71
                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                           MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPHMVTERTVDKSTG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFDKNVSMSSECSTTPSP------
ILGNQGSFLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHNHYTOKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVFVQWQQRGQPLSSDKYVTSAPAPEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFTCTVTHADLPFPLKHTISKSREVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTDLTTYG-SLNISW-----ASHNGKALDTHMNITESHPNATFSAMGEASVCAEDWESGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SSRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR 102
                                                                                                                                                                                    T-cell surface glycoprotein CD4; immunoglobulin
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GKNIQGG-----TCTV----L
                                                                                                                                      13.2%;
98.6%;
71
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                                                                                                                       0,
                                                                                                                                        Score 357;
Pred. No. 5.
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                of the human
PMID:7676667
                                                                                                                                        DB 2;
5.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GIQVFPIAPSFADT-FLSKSARLICL
                                                                                                                                                     Length
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                T-lymphocyte
                                                                                                                                                                                                                                  PID:g1086923
                                                                                                                                                                                    homology
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                                                                                                                       Gaps
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Ig mu chain C region - house shrew (fragment) C;Species: Suncus murinus (house shrew) C;Date: 28-Feb-1990 #sequence\_revision 28-Feb

28-Feb-1990

#text\_change 21-Jan-2000

Τ.,

Nagatsu,

7

Kurosawa, 3

gene

and

comparison

Wit.

A;Title: Nucleotide sequence of Suncus murinus immunoglobulin A;Reference number: S03961; MUID:89232144; PMID:2497033

R; Ishiguro, H.; Ichihara, Y.; Namikawa, FEBS Lett. 247, 317-322, 1989

C; Accession: S03961

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A; Experimental source: C; Genetics:
                    S
                                                                                                                              A;Map position: 6
C;Superfamily: immunoglobulin C region; immunoglobulin C;Superfamils: immunoglobulin C;Keywords: immunoglobulin F;234-305/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                         C;Accession: S25644
R;Parker, K.; Bugeon, L.; Soulillou, J.P.
submitted to the EMBL Data Library, September 1992
                                                                                                                                                                                                                                                                                                                                                              RESULT 74

$25644

Ig mu chain C region - rat (fragment)

G; Species: Rattus norvegicus (Norway rat)

C; Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000

C; Accession: $25644
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A; Residues: 1-343 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X13920 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S03961
A;Molecule type: DNA
A;Residues: 1-457 <ISH>
                                                                                                                                                                                                                                                                                           A;Accession: S25644
                                                                                                                                                                                                                                                                                                        A; Reference number: S25644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: immunoglobulin C region; immunoglobulin; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241-309/Domain:
                                                         Matches
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sir
Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 NYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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122
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                                                         87;
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTISKAKGQPRE-PQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPAATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYVTSNPTPEPONPGLYFVHSILTVSEKDWSSGESFSCVVGHEALPLSVTEKAVDKTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSLSRPKDVANDPPSVFVLPPAQEQLKLRESASITCLVKDFSPPDVFVQWQHHGQPVDPK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISWSRQNGEALQTHVNISESHPNSTFTAKGHASVCREEWESGEKFTCTVQHSDLPSPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALHKGLTFQKNVSSVCMGDDTSTGISVFLLPPTFAN-IFLTQSAQLTCLVTGLATYD-SL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPRTIVMSWLQRGEPVQPSLVSTSAVEAEPKGSGPTTFRVISRLTITENEWLSQREFTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDRADSRRSLWDQGNFPLIIKNLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SSONIY---NFPEVFTGGKYMATSOVLLPSTAILOSTDDYITCHTKHTTGEKEKK
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                           immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin homology <IMM>
                                                                                                                                                                                                                    EMBL:X68312;
ce: spleen
                                                                        13.1%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LG-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ELQVTPELPPNVSIFV---PPR--NSFSGNHPRTSQLICQASGF
                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 354.5; DB 2;
; pred. No. 7.4e-14;
71; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VTLGCLARDFLPRPVTFSWKFKNSSSI------
                                                                      Score 353; DB 2;
Pred. No. 6.4e-14;
                                                                                                                                                                                                                                   NID:g56461;
                                                       Mismatches 107;
                                                                                                                                                                                                                                     PIDN:CAA48392.1; PID:g818025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IEDSDTYI-CEVEDQKEEVQLL 121
                                                                                     Length 343;
                                                       Indels
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F;238-306/Domain: immunoglobulin homology <IMM3>
F;338-416/Domain: immunoglobulin homology <IMM3>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;345-112,139,192,210,238,257,280,326,441/Binding site: carbohydrate (Asn)
F;135-198,245-304,352-414/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lighand disulfide bonds. In some cases, such as IQA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-90/Domain: immunoglobulin homology <IMM1>
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A;Note: the sequence was determined from A;Note: the authors translated the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 13, 5611-5628, 1985
A;Title: Phylogenetic conservation of immunoglobulin heavy
A;Reference number: A02168; MUID:85297761; PMID:2994005
A;Accession: A02168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;McGuire, K.L.; Duncan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Mesocricetus auratus (golden hamster);Date: 30-Jun-1987 #sequence_revision 30-Jun-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mu chain C region - golden hamster
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EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR-EPQVYTLP
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                                                                                                                                                                                                                                         SVFVPSRDAFSGPAPRKSRLFCEASNFSPKQITVSWLRDGKPVKSGFTTEPVTPEDRGSG
                                                                     ----DIQAFPIPPSFVGIFLNKSATLTCLVTNLATYD-TLNISWSSRSGEPLETKTKLTE 276
                                                                                                                                                         PRTYKVISTLTITESDWLNLSVYTCRV--DHRGLTFWKNVSSTCAASPST------
                                                                                                                                                                                                                                                                                                                                P---PKSVLEGSDEYLVCKVHHGNTNKDLRVPIPGVT
                                                                                                                                                                                                                                                                                                                                                                      PLIIKNLKIEDSDTY-ICEVE--DQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
                                                                                                                                                                                                                                                                                                                                                                                                                   VAMGCLARDFLPSSISFSWNYQNKSEV--NQGVRTFPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VELTCTASO--KKSIOFHWKNSNOIKILGNOG--SFLTKGPSKLNDRADSRRSLWDQGNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNTKIMESHPNGTFSAVGVASVCMEDWDNRKEFVCTVTHRDLPSPOKKFISK----PNEV
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                                                                                                             LGGPSVFLFPPKPKDT-LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                               -----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 349; DB 1;
Pred. No. 1.6e-13;
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for residues 105 and 324 as
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RESULT
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Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
A;Title: Amino acid sequence of heavy chain from Xenopus
A;Reference number: A94192; MUID:88176921; PMID:2451244
A;Accession: C31933
Ig gamma-2a chain C region (E5.7A12) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #tex C;Accession: B30503 R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K. J. Immunol. 141, 1754-1761, 1988 A;Title: DNA rearrangements affecting both variable and
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A; Residues: 1-453 < SCH>
C; Superfamily: immunoglobu
C; Keywords: immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig mu chain C region - African clawed frog (fragment) C;Species: Kenopus laevis (African clawed frog) C;Date: 31-Mar-1990 #sequence_revision 30-Jun-1992 #t
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Matches 119
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                                                                                                                                                                                                                                                                                                                                                                     LHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLYSCVV-----EHAESGSLQEKNMSKSLMCDTPITPTSIQVITIPPS-LESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCLATNFTPTHI-----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSF----LTKGPSKLNDRADSRR
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                                                                                                                                                                                                                                                                                               LVKGFYPSDIAVEW--ESNGQPENNYKTTP-----PVLDSDGSFFLYSKLTVDKSRWQQ 404
                                                                                                                                                                                                                                                                                                                                     CADEWNNDK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC
                                                                                                                                                                                                                                                                                                                                                                                                       FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVWD--NIEOFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI
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                                                                                                                                                                                                                              GNVFSCSVMHEALHNHYTQKSLSLSPG-----LQLDETC
                                                                                                                                                                                                                                                              LVKGFSPSEIFVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                        MISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD
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25.8%; Pre-
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Pred. No. 2.5e-13;
'7; Mismatches 189;
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A;Reference number: A30503; MUID
A;Accession: B30503
A;Molecule type: mRNA
A;Residues: 1-112 <GIL>
A;Cross-references: GB:M21925
A;Cross-references: GB:M21925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig neavy chain - nurse shark

C;Species: Ginglymostoma cirratum (nurse shark)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I50731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Vazquez, M.; Mizuki, N.; Flajnik, M.F.; McKinney, E.C.; Kas Mol. Immunol. 29, 1157-1158, 1992
A;Title: Nucleotide sequence of a nurse shark immunoglobulin A;Reference number: 150731; MUID:92357056; PMID:1495502
A;Accession: I50731
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150731
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;469-539/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                             10 LLLVLQLALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQFHWKNSNQ--IKIL
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CEVRHSGSDKSTGMPCPDGFPTALLTVSSSEEIESRKFAIIVCSISDFHSKSISVTW---
                                                                                                                            ----TRRMSGYEYLGGHSGYWGQGTMVTVTTATP--SSPTLYGLVSSCQQGNIDGSVIY
                                                                                                                                                               EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS-----
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                              -ELODSG-
                                                             GCLAMDYSPDVASVTWKKHGQLITTGVQTYPSVRNKKGTYTLS-SQLALIESDAECDQIS
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ilarity 50.0%;
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the codon GAG f
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Pred. No. 5.1e-
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Pred. No. 3.2e-13;
7; Mismatches 22
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A; Cross-references: EMBL: X69492; NID: g62420; PID: g62421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig upsilon chain - axolotl (fragment)
C;Species: Ambystoma mexicanum (axolotl)
C;Date: 13-Jan-1995 #sequence_revision 1
C;Accession: S31436
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                     LDSD--
                                                                                    GQPREPQVYTLPPSRDELTK-NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPV 382
                                                                                                                        EGPEEAAVISEQYIDSDGTFTAMSYLNITKNEWERGDEFTCKVKHFDLPFPLSRSVSKPT
                                                                                                                                                          TKPRE-----EQY---NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                           CADSQTPYQPKVFLIAPKARD-LYIANQPVVICKITKMENSD-SLSVTW-----KRR 259
                                                                                                                                                                                                                              CPELLG--GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                 QKDGQGTFSTTSQINVTKSDWASGDKYTC-----KVEH-----PATSSRAEDTIHN
                                                                                                                                                                                                                                                                                               GKNIQG----GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHT
                                                                                                                                                                                                                                                                                                                                 DTDGNGSIELVCLISGYTPDNIQVRWLVNDKMAPIQGQT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVLGKKGDTVEL-----
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                                                     GRSFAPTMYVFAPHEMELANYDFVSLTCLVKSFSPDDIYIQWKQGKSVIPSDKYVSMEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                        KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYI-----CEVEDQKEEVQL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVF------LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    -----WGTNSYSCSVKH---KPTSTEIHKTITSAECKKATSKPSVQVLQSSCA 121
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%;
                                                                                                                                                                                                                                                                                                                                                                    LVFGLT-----ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPR 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 321.5; DB 2;
Pred. No. 6.3e-12;
5; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558
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RESULT 80
A39016
T-cell surface glycoprotein CD7 precursor -
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 C;Accession: S00980 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. EMBO J. 7, 1979-1988, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A39016; S03520

R;Schanberg, L.E.; Pleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991

A;Title: Isolation and characterization of the genomic human CD7 gene: structural simila A;Reference number: A39016; MUID:91110576; PMID:1703303

A;Accession: A39016
                                                                                             Ig mu chain C region (clone 12022) - horn shark (fragment)
C; Species: Heterodontus francisci (horn shark)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Roywords: glycoprotein; membrane protein; surface antigen; tandem repeat F;1-25/Domain: signal sequence #status predicted <SIG> F;26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT> F;145-180/Region: 9-residue repeats (X-P-P-X-A-S-A-L-P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Aruffo, A.; Seed,
EMBO J. 6, 3313-331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:119770;
A; Map position: 17q25.2-17q25.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:CD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-240 < ARU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Molecular cloning of two CD7 (T-cell leukemia antigen) A;Reference number: S03520; MUID:88111517; PMID:3501369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M37271; NID:g180163; PIDN:AAA51953.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 ISKAKGQP-----REPQVYTLPPSRDELTKNQVSLTCL----VKGFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3313-3316, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-240 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                          ALPDPPAASALPAALAVISFLLGLGLGVACVLARTR 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN--VFSCSVMHEALH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALARGLPGALAAQEVQQSPHCTTVPVGA-----SVNITCSTSGGLRGIYLRQLGPQPQ 67
                                                                                                                                                                                                                                                                                                                             NVYGSGTLVLVTEEQSQGWHRCSDA---
                                                                                                                                                                                                                                                                                                                                                                      NHYTQKSLSLSPGLQLD--ETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTAS 476
                                                                                                                                                                                                                                                                                                                                                                                                                     DI-IYYEDGVVPTTDRRFRGRI-DFSGS---QDNLTITMHRLQLSDTGTYTCQAITEV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEAGTAGLGTYFSYSMLTIQKSDWDKRETFTCVAAHSAV
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Pred. No. 6.2e-12;
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A;Molecule type: mRNA A;Residues: 1-438 <KOK> A;Cross-references: EMBL:X07784; NID:g63963; A;Note: the sequence was determined from the

PIDN:CAA30617.1; PID:g63964 differentiated gene

A; Reference number: S00980; A; Accession: S00980

A; Title: Complete structure and organization of immunoglobulin heavy A; Reference number: S00980; MUID:88328985; PMID:3138109

chain constant

regio

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C;Species: Lepture | Requence | review | C;Date: 04-Sep-1997 | Requence | review | Red | R
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F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;330-400/Domain: immunoglobulin homology <IM4>
F;366,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-474 <WIL>
A; Cross-references: EMBI
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
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                                                                                                   Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g mu chain - Lepisosteus osseus (fragment)
;Species: Lepisosteus osseus
;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 03-Nov-2000
;Accession: I50830
                                                                                                                                                                                                                                  Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395
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                                                                                                                                     Similarity
GKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSDG-SFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NISTQAWLSGAEFYCVVSHQDLPTPLRASIHKEEVKDLREPFVSVLLPPAEDVSAQRFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQGNKV----VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSCVVGHEAIPLKIINRTVNKSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFSCSVMHEALHNHYTOKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTVYTCQVAHQEVTQSRNITGSQVPCS-----IGDPVIKLLPPSIEQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGTWTCTVLQNQKKVEFKI--DIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LEATVTLTCV---VSNAPYGVNVSW-----TQEKKPLKSEIAVQPGEDSDSVISTV
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                                                                                                                                                                                                                           immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                            EMBL: U12455;
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                                                                                                                                 11.4%;
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                                                                                                                                                                                                                                                                                                                            NID:g529949; PIDN:AAC59688.1; PID:g529950
                                                                                                   Score 308.5; DB 2;
Pred. No. 4.2e-11;
2; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
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                                                                                                                                                                                                                               homology
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes in two holostean fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Middleton,
                                                                                                   131;
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                                                                                                   Gaps
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T-cell surface glycoprotein CD4 (allele 1) - pig (f C;Species: Sus scrofa domestica (domestic pig) C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 C;Accession: 147131; S21461 R;Gustafsson, K.; Germana, S.; Sundt, T.M. J. Immunol. 151, 1365-1370, 1993 A;Title: Extensive allelic polymorphism in the CDR2 A;Reference number: 147131; MUID:93329116; PMID:833 A;Accession: 147131
                                                                                                                                                                                                   C;Superfamily: T-cell surface glycoprotein CD4; C;Keywords: glycoprotein; T-cell F;3-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-99 -GUZ>A;Cross-references: EMBL:X65629; N
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61
                               91
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                                                                                                                                    59;
                                                                                                                                                     Similarity
                 NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
                                                                                  KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLDEGVTNIPATVDEKKLYSASSLLTVTEKDWKSSAEFACEFVHKTGSVLKNITYTSREC
                                                                  KAGDLAELPCHSSQKKNLPFNWKNSNQTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSVYSKYTISSSDWNSGTMYSCAVHHETAPLPVSVITRTTDSSTGKATLVNFTLNLPDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFLYSKLTVDKSRWQQGNVFSCSVMHEA-----LHNHYTQKSLSLSPGLQLDETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN-KALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QETV---KVVIEPPTNEEQ-FVKKTATLTCRRIALVSTS----DVSMTWSSGGKPL--AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TPPVPPASVLLNPP----
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SPPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELLGGPSVFLFPPKPKDTLMISRTPEVTC---VVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGNFPLIIKNLKIEDSD-----TYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL 143
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                      EMBL: X65629; NID: g1928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QLSLPTSDWNSGKAFFCEAKHPQGDVKL--
                                                                                                                                                  11.3%; Score 305.5; DB 2 60.2%; Pred. No. 9.7e-12;
                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SLEEFAQNHTATLVCVRSGFSPKTHEFKWWRGNT 180
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                         the CDR2-like PMID:8335933
                                                                                                                                                                                                                                   PIDN:CAA46583.1; PI
CD4; immunoglobulin
                                                                                                                                                                  DB 2;
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98
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                                                                                                                                                                                                                                                      PID: 9388232
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Ig mu chain C region, membrane-bound (clone 3050) - horn shark c;Species: Heterodontus francisci (horn shark) C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change C;Accession: S01854; C32716; Ā46530 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, GEMBO J. 7, 1979-1988, 1988 A;Reference number: S00980; MUID:88328985; PMID:3138109

#text\_change

16-Aug-

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chain

constant

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Ig alpha chain - chicken C; Species: Gallus gallus (C; Date: 18-Jun-1993 #seque C; Accession: A46507 R; Mansikka, A. J. Immunol. 149, 855-861, A; Title: Chicken IgA H cha
                                                                                                                                               RESULT 85
A46507
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F;228-291/Domain: immunoglobulin homology <IMM3>
F;230-400/Domain: immunoglobulin homology <IMM4>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;438-458/Domain: transmembrane #status predicted <TMM>
F;27-85,130-188,235-289,337-398/Disulfide bonds: #status predicted F;164,200,245,275,374,411,415,437/Binding site: carbohydrate (Asm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; 120,107,00main; immunoglobulin; homology <IMM1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: the sequence was determined from the germline gene R;Kokubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. Proc. Natl. Acad. Sci. U.S.A. 84, 5868-5872, 1987
A;Title: Extensive families of constant region genes in a phylogenetically primitive A;Reference number: A32716; MUID:87289703; PMID:3475706
A;Accession: C32716
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A; Residues: 1-99 < KO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 100/1; 206/1; 309/1; 419/1; 459/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X07781
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                                                                                                                                                                                                                                                                       SLSPGLOLDETCAEAODGELDGLWTTDPPRASAL 460
                                                                                                                                                                                                                                                                                                              DKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEAI------
                                                                                                                                                                                                                                                                                                                                                    GQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDGQHMESGFVTSPT--C----GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ 197
                                                                                                                                                                                                                              ---PLKIINRTVNKSSDSS-DHIWIEDNEEESAI
                                                                                                                                                                                                                                                                                                                                                                                                 DLPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFFPREIFVKWTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNAPYGVNVSW----TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSGAEFYCVVNHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
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  855-861, 1992
IgA H chains.
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                                                                             #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
                                                                                                         (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 301.5; DB 1; 26.7%; Pred. No. 1e-10; tive 67; Mismatches 161;
  Implications concerning
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  the evolution
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Nature 374, 168-173, 1995
A;Title: A new antigen receptor gene family that undergoes
A;Reference number: S60266; MUID:95183140; PMID:7877689
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A;Accession: A46507
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-585 <MAN>
A;Residues: 1-585 <MAN>
A;Crose-references: GB:S40610; NID:g251907; PID:g251908
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:109906, NCB
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S60266
R;Greenberg, A.S.; Avila, D.; Hughes, M.; Hughes,
Nature 374, 168-173, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel antigen receptor precursor - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U18701; NID:g699442; PIDN:AAB48195.1; PID:g699443
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic A;Molecule type: mRNA
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                                                                                                                                                   al Similarity
107; Conserv
95
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14; Conservative
                                                VEYTCSAKQDQSSTPVVKRTRKARVEPTKPHLRLLPPSPEEIQSTSSATLTCLIRGFYPD 380
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IIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ 154
                                                                                                VELTCTASQKKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNFPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQPISPQNYLIFGP--EKDGDFYSLYSKLKVSVEDWQRGDVFGCVVGHDGIPLNFIHKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQP--ENNYKTTPPVLDSDGSFF-LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GV-VVAEESIRKETDTPLHAPSVYVFPPPAEELSLQETATLTCMASSFLPSSILLTWTQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 301.5; DB 2; 26.8%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - PAPESDESGCSDCTESGVTQWSRVNVTRKSWEGGAQFGCRVTHGALK--
                                                                                                                                                                            11.2%;
                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                   ; Score 301.5; DB 2; 
; Pred. No. 1.7e-10; 
66; Mismatches 161;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;232-304/Domain: immunoglobulin homology
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Mol. Immunol. 31, 633-642, 1994

A;Title: Characterization of a C alpha gene of swine.

A;Reference number: I47175; MUID:94254897; PMID:7545929

A;Accession: I47175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig alpha chain C region - pig (fragment) c;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change C;Accession: I47175 R;Brown, W.R.; Butler, J.E.
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C;Genetics:
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Best Local
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SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG----LQLDETCAEAQ 442
                                  PSEELALNELVTLTCLVRGFSPKDVLVRWLQGGQELPRDKYLVWESLPEPGQAIPTYAVT
                                                     SRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLY
                                                                                                      DSC-GCYSVSSILPGCADPWNKGETFSCTAAHSELKSALTATITKPKVNTFRPQVHLLPP
                                                                                                                                                                      CC-KPSLSLQPPALAD-LLLGSNASLTCTLSGLKKSE-GVSFTWQPSGGK-DAVQASPTR
                                                                                                                                                                                                        LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
                                                                                                                                                                                                                                                                             QDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH---
                                                                                                                                                                                                                                                                                                             LTLGSSEPAGYVVIACLVRDFFPSEPLTVTWSPSREGVIVRNFPPAQAGGLYTMSSQLTL
                                                                                                                                                                                                                                                                                                                                               LTLTLESPPG-----QGGKTLSVSQLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVLSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVDSEKGSGSSFVTDRLRLTAAEWNSDTTYSCLVGHPSLNRDLIRSTNKSNGKPSSVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-----NHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKANVSQMHPPKVYLLHPSTDEIDTENSATLMCLATNFHPAEIYVGWMANDTLLDSGYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKAK-GOPREPOYTLPPSRDEL-TKNOVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WQVNGVERKKGVETQNPEWSGSKSTIVSKLKVMASEWDSGTEYVCLVEDSELPTPVKASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LINLTAVEWKSGAKYTCTASHPPSQSTVKRVIRNQ-----KVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRSPRGKNIQGGKTLSVSQLELQDSGTWTCT------
                                                                                                                                  EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                           ------PVEQCPADQILKCQVQHLSKSSQSVNVPCKVLPSDPCPQ
                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 300; DB 2; 27.1%; Pred. No. 9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SVSWQKDDVS--VSANVTNFPTAL--EQDLTFSTRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                             -----TCPE
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RESULT 88
S09264
                                                                                                                                                                                                                                                                                                              Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
A;Title: The IGA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
C;Accession: S09264
                                                                            C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin F;142-208/Domain: immunoglobulin homology <IMM>
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-357 < BUR>
                                                                                                                                                                                            A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120 A;Accession: S09269
                                                                                                                                                                                                                                                          C;Accession: S09269
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
                                                                                                                                                                                                                                                                                                                                                                                S09269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: not compared with conceptual translation A;Molecule type: DNA
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                                                                                                                                                                            A; Status: not compared with
                                       Query Match
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                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 LTLESPPGSSPSVQCRSPRGKNIQG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 LQNQKKVEF------KID---IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-339 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALVTLTCLVRGFSPKDVLVYWTNKGVVVPKDSFLVWKPLPBPGQBPTTYAVTSLLRVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q-VSLTCLVKGFYPSDIAVEWESNG--QPENNY---KTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLPGCAETWTAGTEFTCTVTHPEIEGSSLTATIRKDTGSLTPPQVHLLPPPSEELALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKDTLMISRTPEVTCVVVDVSHEDP-EVKFNWYVDGVEVHNAKTKPREEQYN---STYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWNOGDSYSCVVGHEGLAEHFTOKTIDROAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSVLTVLHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLPCPLSGQPVVV-----GCLIQGFFPLGPLNVKWTISGENVTFPPVQLDTSGLYTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRD-LLLGSDASLTCTLRGL--KDPKDAVFTW----EPTNGNEPVQQSPQRDPCGCYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINITDEECPTCVACHVEHNEVDRYLILPCP-----DTHSSCPPTSCGEPSLSLQRPD
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29.0%;
11.0%; Score 296; DB 2;
29.8%; Pred. No. 1.6e-10;
tive 40; Mismatches 104
                                                                                                                                                                         conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 297; DB 2; 1; Pred. No. 1.3e-10; 48; Mismatches 127;
                                                                                                                                                                              translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               320
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                                                                                                                                                                                                                                                                                                                  #text_change
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                                     Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339
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Matches

90;

Conservative

Indels

68;

Gaps

14:

e F 13

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A;Cross-references: GB:K00389; NID:g212204; PIDN:AAA48923.1; PID:g212205
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;49-133/Domain: immunoglobulin homology <IMM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHCH
Ig mu chai
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Nucleic Acids Res. 11, 5381-5389, 1983
A;Title: Nucleotide sequence of the constant region of a A;Reference number: A02170, MUID:83299221; PMID:6310496
A;Accession: A02170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;151-219/Domain: immunoglobulin homology <IMM3>F;258-329/Domain: immunoglobulin homology <IMM4>F;347-367/Domain: carboxyl-terminal <CTS>
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A; Residues: 1-367 < DAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g mu chain C region - chicken (fragment)
;Species: Gallus gallus (chicken)
;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Accession: A02170
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
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                                                                                                                                                                                                                                                                                                                                                         85;
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                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                    VFPPPTEQLNGNQRLSVTCMAQGFNPPHLFVRWMRNGEPLPQSQSVTSAPMAENPENESY
                                                                                                                  -RVLQSNGLYTVDGVATVCASEWDGGDGYVCKVNHPDLLFPMEEKMRKTKASNARPPSVY
                                                                                                                                                                                                                                                                                                                 GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---
                                                                           TLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDS--DGSF
                                                                                                                                                       PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVY
                                                                                                                                                                                              PVVQQDIAIRVITPSFVD-IFISKSATLTCRVSNMVNADGLEVSW-WKEKGGKLETALGK
                                                                                                                                                                                                                                   PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP-EVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                              GPEVVAESRISVTESEWDTGATFSCVV
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FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQNESYTCVVGHEGLAEHFTQRTIDRL 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNS----TYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PG 431
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                          11.0%;
                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                            Score 296; DB 1;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                            Length 367;
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R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09272
A;Status: not compared with conceptual translation
                                                                                                                                                                                   Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan.1993 #sequence_revision 29-Jan-1993
C;Accession: S09272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUX. J. Immunol. 22, 2595-2607, 1992

A;Title: Evolution of vertebrate IgM: complete amino acid sequence A;Reference number: A46532; MUID:93011455; PMID:1382992

A;Accession: A46532
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C;Species: Ambystoma mexicanum (axolotl)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A46532
R;Fellah, J.S.; Wiles, M.V.; Charlemagne, J.; Schwager, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: sequence inconsistent with the nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIP:115354) C; Superfamily: immunoglobulin C region; immunoglobulin homology
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: nucleic acid
A; Residues: 1-454 <FEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Keywords:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQKPNGNQRRKPSVYIYPPPSEELALKETATIVCLMRGYHPCDLFVRWLENSQQLQKQDY
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                                                                                                                                                                                                                                                                                                                                                                                                                VNTKQAEEVDPTTGQKSCFMYSMLKIPAAQWTAGNTYTCVVGHEALPLQITQKSIDRSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTTPPVLDSD-----GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTEITNPIFHD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLLQGQSLTLTLESPPG--SSPSVQCRSP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKAKG-OPREPOVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSMLCDAQVGPVKVTAFTVAFTFEDMFESKSANVTCIVTNMGTIEGFNITWSREDTNEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTHTCPELLGGPSVFLFPPKPK-DTLMISRTPEVTCVVVDV-----SHEDPEVKF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDVTSG--IYTEEPVADTAGNFDVTSLLNIEPMDWNMDTVYSCVVDQTASKFWNTRNMS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPSLGQPLTKKVQFSVQRISKPTVTLHAPAREDIINNNATIVCICRGFHPQPISIKWMKN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYSASTRVKVPSESW------KNRDPYYCKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAQAPSVYPLISCGASLDPVVIGCLAKGFLPDSVTFDWTDKNNASFSAGVAKLPSVTTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATQGNKVV----LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKI----LGNQGSFLTK 71
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23.1%;
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Pred. No. 2.2e-10;
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RESULT
B22360
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C;Superfamily: immunoglo
C;Keywords: immunoglobul
F;232-305/Domain: immuno
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A;Map position: 14q32.33-14q32.33
A;Introns: 1/1 103/1; 210/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Mechanisms of divergence and convergence of the A,Reference number: A94653; MUID:84130179; PMID:6421489 A,Accession: B22360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: B22360
R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, Cell 36, 681-688, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig alpha-2 chain C region (allotype A2m(1)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
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A; Residues: 1-340 <FLA>
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Best Local S
Matches 103
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                                                                                                                                                                                                                                                                                                                                                ;Keywords: immunoglobulin
;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: immunoglobulin C region; immunoglobulin
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  283
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                                                                                                                                                  169 LSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                             122 VFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKT
                                                                                                                                                                                                                                                                       103;
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                                                                                                                TTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPC-----C----H 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIEKTISKAKGQPREPQVYTLPPSRDELTKN-QVSLTCLVKGFYPSDIAVEWESNGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFTWEPTNG----NEFVQQSVQSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHCYCP-PTSC-----GEPSLSLQRPDIGDLLLESKA-SLTCTLSGL--KDPEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENNY - - - KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFNWY-VDGVEVHNAKTKPREEQYN-STYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-A
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                    PRISTHRPALED-LILGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC
                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                           VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKDSYLVWKPLPEPGQDPTTYAVTSLLRVSAEDWNQGDSYSCVVGHEGLAEHFTQRTIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPVPSPSSSLYTT----SSLLSLTDDQCPRDGNVTCHVEHNYDEGQ---DLTVPCQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                       10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 295.5; DB 2
31.7%; Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Mismatches 120;
                                                                                                                                                                                                                                                                     50; Mismatches 143;
                                                                                                                                                                                                                                                                                     Score 294.5; DB 2; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.H.
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                                                                                                                                                                                                                                                                                                         Length 340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human immunoglobulin alpha-1
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                                                                                                                                                                                                                                                                     57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S01853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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427
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SLSPG
                                      DKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEAIPLKIINRTV
                                                                                                                                          ALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                                           KIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                                                                                                                  DLPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFFPREIFVKWTVN
                                                                                                                                                                                                                                                                   SRNITGSQVPC-----SCN------DPVIKILPPSIEQVL-LEATVTLTCV---V
                                                                                                                                                                                                                                                                                                                                                KDGQHMESGFVTSPT--C----GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ
                                                                                                                                                                                                                                                                                                                                                                                    ----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                                                                                                                                                                                                                                                                                                                                                                          RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EDQKEEVQLLVFG--LTANSDTHLLQGQSLTLT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKKDNEPITTG-----LKTYPSVLNKKGTYTQS-----SQLTITESEVGSSKIY-CEVR
                                                                          GQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                           SNAPYGVNVSW----TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSGAEFYCVVNHQ
                                                                                                                                                                                                                               SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
431
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414

354

369

294

237

197

142 88

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into le C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                            F;123-190/Domain: immunoglobulin homology <IM2>
F;228-291/Domain: immunoglobulin homology <IM3>
F;328-291/Domain: immunoglobulin homology <IM4>
F;330-400/Domain: immunoglobulin homology <IM4>
F;364,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete structure and organization of immunoglobulin A;Reference number: S00980; MUID:88328985; PMID:3138109 A;Accession: S01853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig mu chain C region, secreted (clone 3050) - horn shark
C;Species: Heterodontus francisci (horn shark)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 100/1; 206/1; 309/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X07781
A;Note: the sequence was determined from the germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Kokubu, F.; Hinds, K.; Litman, R.; Shamblott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-438 <KOK>
                                                        Query Match
Best Local Similarity
Matches 115; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1979-1988, 1988
WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLPPPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                                           Conservative
                                                                                    10.9%;
                                                           65;
                                                                                       Score 294; DB 1;
Pred. No. 2.8e-10;
                                                           Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.J.; Litman,
                                                                                                             Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                           92;
                                                                                                                                                                                  (covalent) #status
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                                                           Gaps
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   111
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                                                           21
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A/Cross references: GB:X00353; NID:g1575; PIDN:ChA25100.1; PID:g1576
C/Comment: This immunoglobulin belongs to the IgA-g subclass. It was isolated fro C/Complex: An immunoglobulin beterotetramer subunit consists of two identical lig hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C/Superfamily: immunoglobulin C region; immunoglobulin homology C/Superfamily: immunoglobulin homology clusterotetramer; immunoglobulin; plasma F/S6-152/Domain: immunoglobulin homology <NY2>
F/189-261/Domain: immunoglobulin homology <NY2>
F/38,286/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                 A; Molecule type: DNA
A; Residues: 1-338 «BUR»
C; Superfamily: immunoglobulin C
C; Keywords: immunoglobulin
                                                                                                                                                                                                                                              C;Accession: S09276
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Knight, K.L.; Martens, C.L.; Stoklosa, C.M.; Schneiderman, Nucleic Acids Res. 12, 1657-1670, 1984
A;Title: Genes encoding alpha-heavy chains of rabbit IgA: ch A;Reference number: A02174; MUID:84144059; PMID:6322114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
C;Accession: A02174
                                                                                                                                                                                                           A;Reference number: S09264; MÜID:90076124; PMID:2512120 A;Accession: S09276
                                                                                                                                                                                                                                                                                                                                   Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
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A; Residues: 1-299 < KNI>
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Query Match
Best Local S
Matches 92
                                                                                  228-300/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDSGSLTATISRGVVTP---PQVHLLPPPSEELALNEQVTLTCLVRGFSPKDVLVSWRHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSSVLPSSAETWKARTEFTCTVTHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQRPDLGD-LLLGRDASLTCTLSGLK
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                  immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
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                   10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 293; DB 1 31.7%; Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
50;
                                                                                                                         region;
Score 292; DB 2;
Pred. No. 2.7e-10;
0; Mismatches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                     #text_change 16-Jul-1999
                                    Length 338;
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Indels
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40;
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Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_cha
C;Accession: S09266
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning
A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09266
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S09266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-352 <BUR>
A;Residues: 1-352 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;241-314/Domain: immunoglobulin homology <IMM>
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Best Local
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428
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                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                                                                     199 IVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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LSPG
                                                                                                                                                        APIEKTISKAKGOPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGO-- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKN-QVSLTCLVKGFYPSD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                           VPKDSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQGDSYSCVVGHEGLAEHFTQRTID 329
                                                                                                                               GSTTATISRGSTTP--PQVHLLPPPTEELALNALVTLTCLVRGFSPKDVLVSWTHNGTLV
                                                                                                                                                                                                                   AVFTWNPTNGNEFVQQST----QSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEG
                                                                                                                                                                                                                                                              VKFNWY-VDGVEVHNAKTKPREEQYN-STYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-
                                                                                                                                                                                                                                                                                                            PTPCPCP-PITC----
                                                                                                                                                                                                                                                                                                                                                                                                LHNHYTQKSLSLSPG
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                                                                                 - PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAVEWESNGQ--PENNY----KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTCTLSGLKNPEDAV-FTW--EPTNGNEPVOORAORDLSGCYSVSSVLPSSAETWKARTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYNSVINESLPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQRPDLGD-LLLGRDAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPG--PLSVSWTVNGENV---SAYNFPPAQSGTSGPYTACSELILPVTQCLGQKSAACHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 292; DB 2; 31.2%; Pred. No. 2.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                          -GEPSLSLQRPDIGD-LLLESNASLTCTLSGL--KDPEG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 118;
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330 RLAG

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Ig heavy chain precursor V region - ladyfish
C;Species: Elops saurus (ladyfish)
C;Species: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000
C;Accession: A34891
R;Amemiya, C.T.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990
A;Fitle: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and analy A;Reference number: A34891; MUID:90138916; PMID:2105490
A;Accession: A34891
A;Accession: A34891
A;Gross-references: GB:M26182; NID:90138916; PMID:2105490
A;Molecule type: mRNA
A;Residues: 1-568 <AME>
A;Gross-references: GB:M26182; NID:9213134; PIDN:AAA49238.1; PID:9213135
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
                                                                              Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
C;Dates 39-265
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The 1gA heavy-chain gene family in rabbit: cloning and
A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-357 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;246-319/Domain: immunoglobulin homology <IMM>
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Matches 92
    Query Match
Best Local S
Matches 93
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    th 10.7%; similarity 28.2%; 93; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOFDE-OKMISKLLIDYEEWKNRTEYTCKVEHSDLPSPLRTSYRRECGGKWQSPTVFILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TASSFLQASESQWKRLDGTFTCQFIQEGEITEQTVKYSSAEC-SPEAQIDAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATFACLATD-----FYPKGHSFKWLRDGKEVT-----DGIATLTECQKKGDKSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA-EQRNLSTVTLICYAKDFYPEQVLISWLVDDQPVETDVPTTEVVKTEGTYSVFSQLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE--VHNAKTKPRE
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      49;
    Score 289; DB 2; pred. No. 4.3e-10; 9; Mismatches 122;
                                                                                                                                                                                                                                                                                                                       #text_change 16-Jul-1999
                                       Length 357;
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    Gaps
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      14;
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence
C;Accession: I56230
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C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 102;
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Best Local .
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                                                                                                                                            168
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                                                                                                                                                                                                                                                                                                                                         169 LSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
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VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                                                                               STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                             PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                           LALNELYTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILR
                                                                                                    LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
                                                                                                                                            GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLPPPSEE
                                                                                                                                                                                                                      PRISIHRPALED-LILGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC
                                                                                                                                                                                                                                                                                                                                                                                  VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
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396

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A;Introns: 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin
F;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                             R;Chintalacharuvu, K.R.; Raines, M.; Morrison, S.L.
J. Immunol. 152, 5299-5304, 1994
A;Title: Divergence of human alpha-chain constant region
A;Reference number: 156230; MUID:94246170; PMID:8189047
A;Accession: 156230
                                             122 VFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKT 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LQGQSLTL-TLESPPGS-------SPSVQCR---SPRGKNIQGGKTLSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP
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                                                                                                                 Score 286.5; DB 2;
Pred. No. 5.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                       GB/EMBL/DDBJ
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Db 287 VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC 339
Search completed: August 3, 2004, 13:15:19
Job time: 16.7668 secs

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Result
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Maximum Match 100%
Listing first 125 summaries
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Perfect score:
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-09-409-006A-4
US-08-484-681-4
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PCT-US95-00454-5
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US-09-517-605-3
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Sequence 5, Appli Sequence 29, Appli Sequence 29, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3
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GENERAL INFORMATION:
                                                                                                                                                           APPLICATION NUMBER: US/08/472,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/618,314
APPLICATION NUMBER: 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/258001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICANT: Walz, Gerd
TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS
TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Clark & Elbing LLP
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
                    TYPE: amino acid
STRANDEDNESS: unl
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US-09-26-985-71
US-09-234-340A-71
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US-08-477-460B-4
                                                                                                                                                               Sequence 4, Application US/08477460B
Patent No. 6034223
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
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Best Local (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                             JAKEET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                  COUNTRY: US
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Pred. No. 5.1e-245;
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Best Local Similarity 68.9%;
Matches 437; Conservative
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acids
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 412
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                --VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                        ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 471
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                                                                                                            EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                                                                                                            EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 531
                                                                                                                                                                                                                                                                                                                                                                                             QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL
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                                                                                                                                                                                                                                                                                                    TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV------
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Pred. No. 7.3e-160;
5; Mismatches 58;
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CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER FILING DATE: 1993-08-06
EARLIER APPLICATION NUMBER: 07/927,931
EARLIER FILING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2:1
SEQ ID NO 4
LENGTH: 530
TYPE: PAT
ORGANISM: Homo sapiens
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US-08-379-516-4
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Best Local S
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APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 591
                                                                                                                                    EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
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RESULT 4
US-09-329-916-4
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Best Local Similarity
Matches 437; Conser
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APPLICATION NUMBER: 08/477,46
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
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CITY: New York
STATE: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
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                                         TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240
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                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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Pred. No. 7.3e-160;
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; Patent No. 6187748
; GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                     APPLICATION NUMBER: 08/476,22
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
08/476,227
                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                 TOPOLOGY: unknown
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                                                                                           LENGTH:
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                                                                       amino acid
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1185 Avenue of the Americas
                                                                                         530 amino acids
                                                                                                                                                                       (212) 391-0525
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                                                         unknown
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; ORGANISM:
; CELL TYPE:
US-08-485-372A-4
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US-09-409-006A-4
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Best Local Similarity
Matches '437; Conserv
ZIP: 10112
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              APPLICANT: Progenics Pharmaceuticals, TITLE OF INVENTION: NON-PEPTIDYL MOIETTITLE OF INVENTION: CD4-GAMMA2 AND CD
                                                                                                                        NUMBER OF SEQUENCES: 9
                                                                     STREET: 30 Rockefeller Plaza CITY: New York
                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                 592
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                                                                                                                                                NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES,
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Pred. No. 7.3e-160;
5; Mismatches 58;
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Best Local
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 29-SEP-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unl
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lymphocyte
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TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 530 amino acids
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APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                           EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 531
                                                                                                                                                                                                                                                                                                                                                                  ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP 411
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                                                              PSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPMLDSDGSFFLYSKLTV
                                                                                                 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 591
                                                                                                                                                                                  EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
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Pred. No. 7.3e-160;
Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.0%; Sometime 68.9%; Published 437; Conservative 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/08/484,681
CURRENT APPLICATION UNMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bequence 4, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 530 amino acids
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ORIGINAL SOURCE:
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TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
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STREET: 1185 Avenue of the Americas
CITY: New York
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                                   241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL 297
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Pred. No. 7.3e-160;
5; Mismatches 58;
-PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 255
                                                                             -KGPSV---FPLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 530;
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PICATION PILICATION PI	RESULT 8  PCT-US93-07422-4  Sequence 4, Application PC/TUS9307422  GENERAL INFERMATION:  APPLICANT: Progenics Pharmaceuticals, Inc.  ITILE OF INVENTION: NON-PEPTIDYL MOLETY-CONJUGATED  TITLE OF INVENTION: CD4-GAMMAZ AND CD4-IGCZ IMMUNOCONJUGATES, AND USES THER  NUMBER OF SEQUENCES: 9  CORRESPONDENCE ADDRESS:  ADDRESSEE: Cooper & Dunham  STREET: 30 Rockefeller Plaza  CITY: New York  STATE: New York  COUNTRY: USA  ZIP: 10112  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.24  CURRENT APPLICATION DATA:  APPLICATION DATA:  PCT/US93/07422	592 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625	532 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV 591    : :	472 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 531    :   :	412 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 471	357 PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCP 411	298 TLALEAKTGKLHQEVNLLVVMRATQL-QKNLTCBVWGPT8PKLMLSLKLENKEAKVSKREK 356

Query Match

62.0%;

Score 2116;

DB 5;

Length 530;

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RESULT 9
US-08-477-460B-2
                                                                                                                                                                                                                                                                       Sequence 2, Application US/08477460B
Patent No. 6034223
GENERAL INFORMATION:
APPLICANT: Progenice Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
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                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PM PC FOOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                           STREET: JOIK
CITY: New York
TATE: New York
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaz
             APPLICATION NUMBER: US/OFILING DATE: 07-JUN-1995
                                                                                                                                               ZIP: 10112
CLASSIFICATION:
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                            US/08/477,460B
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5; Mismatches 58;
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ORIGINAL SOURCE:
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CELL TYPE:
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STRANDEDNESS: unl
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                                                                                                                                                                                                VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
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                                                                     VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                     QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                               QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
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lymphocyte
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APPLICANT: Allawy, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: NO. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER APPLICATION NUMBER: 07/927,931
EARLIER FILING DATE: 1993-08-06
EARLIER FILING DATE: 1993-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                          QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                             LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
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                                VFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                     VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
                                                                                                                                                                       VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 540
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                                                                    QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
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RESULT 11

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-P(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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; Patent No. 6177549
; GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unl
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   241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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                                       TWTCTVLQNQKKVEFKIDIVVLAFERKCCV---
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Pred. No. 1.8e-155;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                                                                                                                                                                                                                                                                               Indels 194;
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RESULT 12
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APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2
 -08-485-372A-2
                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-I
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,37:
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                            TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
             CELL TYPE:
                                                                                                                            LENGTH: 432 amino acids
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1185 Avenue
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RESULT 13
US-09-409-006A-2

Sequence 2, Application US/09409006A

Patent No. 6342586

GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceutical
TITLE OF INVENTION: NON-PEPTIDYL M
TITLE OF INVENTION: CD4-GAMMA2 AND
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                                                                                                                                           STREET: JV
STREET: New York
CITY: New York
TTATE: New York
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/09/409,006
FILING DATE: 29-SEP-1999
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          ADDRESSEE:
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30 Rockefeller Plaza
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NON-PEPTIDYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IgG2 IMMUNO
                 US/09/409,006A
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Best Local (
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFAX: (212) 977-9809
TELEFAX: 02523 GOOP UI
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0.
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
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               VFSCSVMHEALHNHYTQKSLSLSPG
                                                                           QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                       VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
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                                                                                                                      VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
                                                                                                                                                                                                LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
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VFSCSVMHEALHNHYTQKSLSLSPG
                                                            QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2059; DB 4;
Pred. No. 1.8e-155;
2; Mismatches 9;
431
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; ORGANISM: (; CELL TYPE: US-08-484-681-2
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Best Local Similarity
Matches 410; Conserv
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APPLICANT: Beaudry,
APPLICANT: Maddon,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn ReleacCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 07-UN-1999
CLASSIFICATION: 435
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STREET: 1185 Avenue of the
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 432 amino acids TYPE: amino acid STRANDEDNESS: unknown
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   301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
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                                                                                                                                                                                 121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                     121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                          61 ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                       61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
lymphocyte
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CD4-GAMMA2 CD4-IgG2 CHIMERAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
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PCT-US93-07422-2
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                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-950
TELEPAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceutics
TITLE OF INVENTION: NON-PEPTIDYL P
TITLE OF INVENTION: CD4-GAMMA2 ANI
NUMBER OF EQUENCES:
CORRESPONDENCE ADDRESS:
                                                Matches 410;
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHATION Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 1930806
CLASSIFICATION:
                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: unkn
MOLECULE TYPE: p
ORIGINAL SOURCE:
ORGANISM: homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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  1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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T: 30 Rockefeller Plaza
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Progenics Pharmaceuticals, Inc.

VENTION: NON-PEPTIDYL MOIETY-CONJUGATED

VENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES
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                                                   Conservative
                                                                                                                                                                                                                                                             unknown
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lymphocyte
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                                                                                                                                                                                                                                                                                   unknown
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                                              Score 2059; DB 5;
Pred. No. 1.8e-155;
2; Mismatches 9;
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                                                                                       Length 432;
                                              Indels 194;
                                              Gaps
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US-08-417-495-6
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APPLICANT: Seed, Brian et al.
                                                                                                                                                                                                                                                                    CILL
STATE: FL.
STATE: USA
COUNTRY: USA
TTP: 02110-2804
TTP: TRADABLE F
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 model 50
OPERATING SYSTEM: IBM P.C.
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCE: ADDRESS:
CORRESPONDENCE ADDRESS:
Pish & Richardson
Processes:
Procedure Address
Pr
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: E
                                                                                          APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601
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  US/07/847,566
                                              US/08/203,866
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CUMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PC. DOS (Version SOPTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
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US-08-284-391B-6
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                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Seed, Babak
APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CEILS BY CHIMERIC CD4 RECEPTOR- BEARING CEILS
TOTAL OF SEQUENCES: 53
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Best Local S
                                                                                                                                                                                                                                                                 Sequence 6, Application US/08284391B Patent No. 5851828
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
COMPUTER READABLE FORM:
             STREET: 176 F.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
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Local Similarity 98.3%;
nes 397; Conservative
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REGISTRATION NUMBER: 30,162
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APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION: 435
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                                                                                176 Federal Street
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RESULT 18 US-09-218-950-6

360 360 300 300

Sequence 6, Application US/09218950 Patent No. 6284240

GENERAL INFORMATION:
APPLICANT: Seed, B:
APPLICANT: Banapous
APPLICANT: Romeo, (

Romeo, Charles Seed, Brian

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Matches 397;
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Best Local Similarity 98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acid
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PRIOR APPLICATION UMBER: 08/195,399

APPLICATION NUMBER: 07/847,569

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 07-MAR-1992

APPLICATION NUMBER: 07/65,96:

APPLICATION NUMBER: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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SOFTWARE: FASESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
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TELEX:
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                     361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
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                                                                                                                                                               241 QAERASSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                     LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPKLC
                                                                              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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Pred. No. 1.5e-153;
1; Mismatches 3;
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FABISEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
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MEDIUM TYPE: Diskette
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CORRESPONDENCE Clark & Elbing LLP

ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kolanus, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/1
FILING DATE: 14-FEB-1994
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97; Conservative
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                                                            QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                           QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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                             LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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VENTION: TARGETED
VENTION: CELLS BY
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98.3%;
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Pred. No. 1.5
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leg 3;
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PCT-US92-01785-6
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Matches
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/66
PILING DATE: March 7, 199
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Versi
SOFTWARE: Wordperfect (Version 5.0)

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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TELEFAX: 200154
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                                                                                                                                                                                                                                                                                                                              Local Similarity
les 397; Conserv
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STREET: 225 Franklin Street
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                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                   TWTCTVLQNQKKVEFKLDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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Pred. No. 1.5e-153;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                Query Match
Best Local
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APPLICATION NUMBER: 07/665
FILING DATE: March 7, 1991
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OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Targeted Cytol TITLE OF INVENTION: Cells by Chime TITLE OF INVENTION: Bearing Cells
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5" Diskette,
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/247001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/847,566 FILING DATE: March 6, 1992
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                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                Score 2036.5; DB 5;
Pred. No. 1.5e-153;
1; Mismatches 3;
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                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                  Indels
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Patent No. 5843728
                 Best
 Matches
                                Query Match
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                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PC. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seed, Brian et al. TITLE OF INVENTION: Redirecti TITLE OF INVENTION: Receptor NUMBER OF SEQUENCES: 27
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                 MOLECULE TYPE:
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                                                                                                                                                                     TELEFAX: 10-
TELEFAX: 200154
                                                                                                                    LENGTH:
TYPE: a
   Local Similarity
les 397; Conser
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: March
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                                                                                                    TOPOLOGY:
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                                                                                                 1: 575 amino acids
   amino acid
   GY: linear
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225 Franklin Street
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llarity 98.3%;
Conservative
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   1;
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Score 2036.5; DB 2;
Pred. No. 1.7e-153;
1; Mismatches 3;
   Indels
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RESULT 22
US-08-284-391B-4
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                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REGISTRATION NUMBER: 00786/2

TELEPHONE: 617-428-7045

TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldema
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 575 amino acid
                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF
TITLE OF INVENTION: CELLS BY CHIMERIC CD4
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: BC
STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                              FILING DATE: 07
CLASSIFICATION:
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                                                          TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 Federal Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
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                                                                                                                             00786/247001
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RESULT 23
US-09-218-950-4
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Patent No. 6284240
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Best Local Similarity
Matches 397; Conserv
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEJ
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,3
APPLICATION NUMBER: 08/195,395
APPLICATION NUMBER: 08/195,395
FILLING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                       STREET:
CITY: Bo
STATE: M
COUNTRY:
                                                                                                 CLASSIFICATION:
                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                            COMPUTER:
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STRANDEDNESS: siz
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98.3%;
                                                                US/08/284,391
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Pred. No. 1.7e-153;
1; Mismatches 3;
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RESULT 24
PCT-US92-01785-4
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                                                                                                                                                            Sequence 4, Application PC/TUS9201785

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation

TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor

TITLE OF INVENTION: Chimeras

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-7045
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 575 amino acids
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
COMPUTER: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
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Local Similarity 98.3%;
1es 397; Conservarium
                                                                                                               COUNTRY:
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TOPOLOGY: lir
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Pred. No. 1.7e-153;
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: AMINO ACID
                                                                                                                                                                Sequence 4, Application PC/TUS9500454
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Targeted Cytol
TITLE OF INVENTION: Cells by Chime
TITLE OF INVENTION: Bearing Cells
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
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APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                             NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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                                                      STREET: __
STREET: __
STRY: Boston
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                                                                                             225 Franklin Street
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98.3%;
                                                                                                                                                                                       Targeted Cytolysis of HIV-Infected Cells by Chimeric CD4 Receptor-
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Pred. No. 1.7e-153;
1; Mismatches 3;
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; Sequence 5, Application U, Patent No. 5843728; GENERAL INFORMATION: APPLICANT: Seed, Bria: TITLE OF INVENTION: R; TITLE OF INVENTION: R
                                                                                                           RESULT 26
US-08-417-495-5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
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FILING DATE: March 7, 1991
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                                    Brian et al.
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98.3%;
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Receptor
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                  of Cellular Immunity
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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NAME: Clark, Paul T.
REGISTRATION UNMBER: 30,162
REFERENCE/DOCKST NUMBER: 0076
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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APPLICATION NUMBER: 1
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APPLICATION NUMBER: US/07/847,566
FILING DATE: March 7, 1991
CLASSIFICATION: 435
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ZIP: 02110-2804
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CITY: Boston
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Similarity 98.0%;
LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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Pred. No. 2.6
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Best Local Similarity
Matches 396; Conserv
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GENERAL INFORMATION:
APPLICANT: Seed, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 462 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/284,391B FILING DATE: 02-AUG-1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/195,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Diskette
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ADDRESSEE: Clark & Elbing LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elbing, Karen L
REGISTRATION NUMBER:
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Pred. No. 2.6e-153;
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US-09-218-950-5
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       Query Match
Best Local Similarity
Matches 396; Conser
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/:
FILING DATE: 02-AUG-1994
APPLICATION UMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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APPLICANT: I
APPLICANT: I
APPLICANT: I
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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CRASSIFICATION DATA:
PRIOR APPLICATION DATA:
US/08/284,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ANDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                           NAME: Elbing, Karen L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/218,950 FILING DATE:
                                                                                                              TOPOLOGY:
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                                                                                                                                                                 LENGTH:
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                                                                                                                                                                 462 amino acids
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       59.5%;
nilarity 98.0%;
Conservative
                                                                                                            ESS: single
linear
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Romeo, Charles
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       2;
       Score 2032.5;
Pred. No. 2.6e
2; Mismatches
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5; DB 3;
2.6e-153;
3;
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                                                                      TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-01785-5
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PCT-US92-01785-5
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Sequence 1, Applicant: The General Hospital
APPLICANT: The General Hospital
TITLE OF INVENTION: Redirection
TITLE OF INVENTION: Chimeras
REQUENCES: 27
Query Match 59.5%;
Best Local Similarity 98.0%;
Matches 396; Conservative
                                                                                                                                                         TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" biskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01785
FILING DATE: 19920306
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                           NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/60
FILING DATE: March 7, 199
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-28
                                                                                                                                                                                                TELEPHONE: (617) 542-8906
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                                                                                                                                          LENGTH:
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                                                                                                                         AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                         07/665,961
                                                                                                                                                                                                                                                                                                                                          1991
Score 2032.5; DB 5
Pred. No. 2.6e-153;
2; Mismatches 3;
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                               DB 5;
 Indels
                                 Length
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               LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
                                                                          LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                   QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPQLC
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                                                        LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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RESULT 30
PCT-US95-00454-5
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GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
                                                  APPLICATION NUMBER: 07/665,96
FILING DATE: March 7, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        CUMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: March 6,
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 Model 50
OPERATING SYSTEM: IBM P.C.
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00454-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-284-391B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5851828
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seed, BILLING APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
FILING DATE: 10-FEB-1994
FILING DATE: 10-FEB-
APPLICATION NUMBER: 07/8 FILING DATE: 06-MAR-1992 APPLICATION NUMBER: 07/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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Similarity 98.0%;
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176 Federal Street
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Pred. No. 2.6e-153;
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Sequence 29, Application US/0921895
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CY
TITLE OF INVENTION: CELLS BY CH
NUMBER OF SEQUENCES: 53

CYTOLYSIS OF HIV-INFECTED CHIMERIC CD4 RECEPTOR- BE

BEARING CELLS

Application US/09218950

COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

STATE: MA CITY: Boston

CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street

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RESULT 32
US-09-218-950-29
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-428-7045
                                                             361
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                                                                                                                                                                                                                                                                               181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                               361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                                                                                                                                       241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                     241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394;
                                                                                                                                                                                                                                                                                                                                                                              61 ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                          LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV
                                                                                                                                            LEAKTGKIHQEVNI VVMRATQIQKNI TCEVWGPTSPKIMISI KLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                          LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                     TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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Pred. No. 4e-153;
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RESULT 33
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                                                      Sequence 4, Application US/08466368 Patent No. 6093539 GENERAL INFORMATION:
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Best Local (
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FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
   APPLICANT:
APPLICANT:
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SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION
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TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: 811
TOPOLOGY: linear
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Maddon, Paul J.
Littman, Dan R.
Chess, Leonard
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Matches 394;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/466
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: McDougal, J. S.
TITLE OF INVENTION: DA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TRI
NUMBER OF SEQUENCES: 21
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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STATE: New York
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361
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                                                                  LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                        QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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100.0%; Fi
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RESULT 34 US-08-328-500-9 ; Sequence 9, Application US/08328500

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TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
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APPLICANT: Maddon, Paul APPLICANT: Axel, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sweet, Richard W.
APPLICANT: Arthos, James
TITLE OF INVENTION: DERIVATIVES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
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CITY: New York
STATE: New York
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361
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                                                                                      LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                          QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                                                                                                                                                                                                                                                    | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                  LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                        QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                         TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
 INPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWV
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99.7%;
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Pred. No. 2.1e-152;
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RESULT 35

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                                                                                                                                                                                                                                                                                                                                                                                       Matches 392;
                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415/225-189
TELEPAX: 415/925-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
PRIOR APPLICATION NUMBER: 07/250785
APPLICATION NUMBER: 07/250785
APPLICATION NUMBER: 07/250785
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MEDIUM TYPE: 5.25 inch, 360 Kb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-SEP-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 402 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                        241
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                                                                                                                                                                        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                    61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                            1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                            ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                  TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFFLAFTVEKLTGSGELWW
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Pred. No. 3.6e-152;
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US-08-457-918-1
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                                                                     Query Match
Best Local Similarity
Matches 392; Conserv
                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                              NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: (
FILING DATE: 28-SEP-1
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
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FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 5.25 inch,
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
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FILING DATE: 1-JUN-1995
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MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                       Conservative
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                                                                     Score 2017; DB 3;
Pred. No. 3.6e-152;
0; Mismatches 1;
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                                                                                                        Length 402;
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RESULT 37
US-09-039-555B-15
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US-09-039-555B-15
                                                             LELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino
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                                                                                                                                                                                                                  CLASSIPICATION: 514

RRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197

FILING DATE: 14-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 2000,-Jan.
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PROMOTER OF THE
TITLE OF INVENTION: PREPARATION AND
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-H
            MOLECULE TYPE:
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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CITY: Washington
                             TOPOLOGY:
                                             STRANDEDNESS
                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/039,555B FILING DATE: 16-MAR-1998
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                                                                               458 amino acids
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USE
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Length 458;

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US-09-517-605-3
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Best Local S
Matches 392
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APPLICANT: Kitman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Wan Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 458
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09517605 Patent No. 6391567
                                                                                                                                                                                                                                  Matches 391;
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
-09-517-605-3
                                                                                                                                                                                                                                                Local
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Pred. No. 6.3e-152;
0; Mismatches 2;
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                                                                                                                                                                                                                                                Score 2007; DB 4; Length 458; Pred. No. 2.7e-151;
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Matches
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                                                                                                                                                                                   Query Match
Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,368

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER 6 PROTEIN
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APPLICANT:
APPLICANT:
APPLICANT:
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STREET: LLU-
CITY: New York
CTATE: New York
TISA
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                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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                                                    61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                 ILGNQGSSLTKGPSKLNDRADSRRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVQL
                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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Chess, Leonard
Axel, Richard
                                                                                                                                                                                                                                                                                                       394 amino acids
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Littman, Dan R.
                                                                                                                                                                        Conservative
                                                                                                                                                                                     58.6%;
98.7%;
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                                                                                                                                                                   Score 2001; DB 3;
Pred. No. 6.6e-151;
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; Sequence 2, Application US/08328500
; Patent No. 6673896
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; APPLICANT: Axel, Richard M.
APPLICANT: Sweet, Richard W.
; APPLICANT: Arthos, James
; TITLE OF INVENTION: DERIVATIVES O
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US-08-328-500-2
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/24577-CY
                                                                                                                                                                                                                              Query Match
Best Local S
Matches 389
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
ILGNOGSSLTKGPSKLNDRADSRRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVQL
                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                                                                                                                                                                                                      Score 2001; DB 4;
Pred. No. 6.6e-151;
                                                                                                                                                                                                                              Mismatches
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NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
                                                                                                                                                                                                                                                                                                                                                           Best Local Sim: Matches 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                               LEAKTGKLHQEVNLVVMRHTQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWV
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV
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Pred. No. 7.4e-150;
0; Mismatches 6;
394
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RESULT 42 5223418-2 ; Patent No.

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RESULT 43
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TITLE OF INVENTION: METHOD OF IMPROVING THE YIELD OF
;HETEROLOGOUS PROTEINS PRODUCED BY STREPTOMYCES LIVIDANS
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ARCURI, EDWARD J.; BRAWNER, MARY E.; DONOVAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 28-SEP-1990
NO:2:
                                                          CLASSIFICATION:
                                                                      APPLICATION NUMBER: US/08/236,311 FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                    STREET:
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APPLICATION NUMBER: 07/936190 FILING DATE: 26-AUG-1992
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South San Francisco
California
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Pred. No. 6.2e-147;
0; Mismatches 10;
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Sequence 4, Application US/08457918
Patent No. 6117655
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variar
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

/ J. Nariants

STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California

COUNTRY:

USA

94080

US-08-457-918-4

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Best Local Similarity
Matches 369; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 28-SEP-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
416 IKVLPTWSTP
                                                                                                  324 KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESN
                                    384 IKVLPTWSTP
                                                                                                                                                       296
                                                                                                                                                                         264 KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ
                                                                                                                                                                                                                                 236 FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                              176 ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA
                                                                                                                                                                                                                                                                                                                                  144 ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA
                                                                                                                                                                                                                                                                                                                                                                                        116 RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                84 RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 434 amino acide amino acid
                                                                                                                                                                                                                                                       FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
                                                                          KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLESN
                                                                                                                                                       KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ
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Pred. No. 3.9e-143;
0; Mismatches 1;
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/842
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/250
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/104
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 07/104
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
ADME: Tofficers
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OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/457,918 FILING DATE: 1-JUN-1995 CLASSIFICATION: 435
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          416
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                              IKVLPTWSTP 393
                                                                                                                                                     KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ 323
                                                                                                                                                                                                                    FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV 263
                                                                                                                                                                                                                                                                                 ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA 203
                                                                                                                                                                                                                                                                                                                                RSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL 175
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                                                                                                                                                                                                                                                                                                                                                                                              QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR 115
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          IKVLPTWSTP 425
                                                                                            KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESN 383
                                                                                                                                                                                                  FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
                                                                                                                                                                                                                                                                  ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA
                                                                      KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLESN
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Best Local S
Matches 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
TOPOLOGY: linco
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 28-Feb-1997
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CITY: New York
      326
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RESULT 45

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GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Antibody;
TITLE OF INVENTION: Antigen COTITLE OF INVENTION: Protection
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue TELEFAX: (212)751-849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/657,149
FILING DATE: 03-June-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARTIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: #1.25
CURRENT APPLICATION DATA: 301 26 NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS 1 NKVVLGKKGDTVELTCTASQKKSIQFHWKNWNQIKILGNQGSFLTKGPSKLNDRADSRRS LMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK 385 VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWIIFDLKNKEVSVKR PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKR VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN PatentIn Release #1.0, 55.4%; Score 1892; DB 2; 99.5%; Pred. No. 3.5e-142; Antibody Against a Host Cell Antigen Complex for Pre- and Protection from Infection US/08/867,149 0; Mismatches 1151-4145 Length 433; Post-Exposure HIV Primary Isolates 0 Gaps 325 145 360 300 240 265 180 205 120 60 0

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US-08-808-374-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Antibody Against a Host Cell
TITLE OF INVENTION: Antigen Complex for Pre- and
TITLE OF INVENTION: Protection from Infection by
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (212)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/657,149
FILING DATE: 03-June-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 28-Feb-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Maria C.H. Lin
                                                   181
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                                                                                                                 121
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                     266
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                                                                                                                                                                                                                                                                                                              367;
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                                                                                                                                                                                                                                                                           26 NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
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                                                                                                                                                                                                                                                                                                                              Similarity
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VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN
                                                                              KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKR 265
                                                   KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWIIFDLKNKEVSVKR
                                                                                                                 PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ
                                                                                                                                               PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ 205
                                                                                                                                                                                                                                                 NKVVLGKKGDTVELTCTASQKKSIQFHWKNWNQIKILGNQGSFLTKGPSKLNDRADSRRS
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                                                                                                                                                                                                                                                                                                                            Score 1892; DB 2;
Pred. No. 3.5e-142;
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                           Length 433;
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HIV Primary I
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US-09-100-409A-1
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GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Chang Yi TITLE OF INVENTION: PEPTII TITLE OF INVENTION: PREVEN TITLE OF INVENTION: IMMUNE
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 345 Par
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                            207
                                                                                          147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN
                                                                                                                       62
                                                                                                                                                   87
                                                                                                                                                                                                   27 KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL
                                                                                                                                                                                                                                              366;
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                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK 360
                              ASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRV 266
                                                                            PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQK 206
                                                                                                                       WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                                                                                                        WDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLTESF 1.46
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#1.25
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                                                                                                                                                                                                                                                          Score 1887; DB 3; Pred. No. 8.7e-142;
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RESULT 49
US-08-630-172-17
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; APPLICANT: CHIBA, YUKINOBU
; TITLE OF INVENTION: LEUJA BINDING PEPTIDES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/526,921
; FILING DATE: 22-MAY-1990
;SEQ ID NO.13:
; LENGTH: 433
                                               GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVE
TITLE OF INVENTION: LYMP
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.6%; Best Local Similarity 91.2%; Matches 342; Conservative
                                                                                                                                                                            Sequence 17, Application US/08630172
Patent No. 6060054
                  STREET:
Denver
: Colorado
                                                                                                                                                                                                                                                                                                            LESNIKVLPTWSTPV 394
                                                                                                                                                                                                                                                                                                                                                                                      TQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQIKILGNXGSF-LTKGPSKLNDRADS-----RRSEEVQLLVFGLTANSDTHLLQGQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVVLGKKGDTVELTCTASOKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS- 85
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                                                                                                                                                                                                                                                                                          LESNIKVLPTWSTPV 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNK
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                                 E: Sheridan Ross & McIntosh
1700 Lincoln Street, 35th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369
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                                                                                                         NOVEL PRODUCT AND LYMPHOCYTE VETO
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Pred. No. 1.6e-126;
5; Mismatches 13;
                                                                                                                            PROCESS
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RESULT 50
US-09-375-419-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COUNCIL GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                               ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQ 565
                                                                                                                                                                                                                                   SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 505
                                                                                                                                                                                                                                                                                        PCP----PCKCPA------PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDV
                                                                                                                                                                                                                                                                                                            VLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
                                                                                                                                           DLPAPIERTISKPKGSVRAPQVYVLPPP-EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGK
                                                                                                                                                                                                                SEDDPDVQISWFVNNVEVHTAQTQTHREDYNSRLRVVSALPIQHQDWMSGKEFKCKVNNK
                                                                                                                                                                                                                                                                                                                                                                                                 LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1585.5; DB 3; ; Pred. No. 7.3e-118; 33; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #1
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.4%; Score 1585.5; DB 3; Best Local Similarity 54.2%; Pred. No. 7.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Connell, Gary J.
REGISTION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Denver
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               VLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 445
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                                                                                                                                                                 VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN 325
                                                                                                                                                                                                                                                                                    PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ 205
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                                                                                                                                                                                                                                                                   PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDAGTWICTVLQNQKKVEFKIDIVVLA--
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1700 Lincoln Street, 35th Floor
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 PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDV
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;Patent No. 5223394
;Patent No. 5223394
; APPLICANT: WALLNER, BARBARA
; TITLE OF INVENTION: RECOMBINA
;LYMPHOCYTE FUNCTION-ASSOCIATED AN
;LINKAGE SIGNAL SEQUENCE
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA;
; APPLICATION NUMBER: US/07;
; FILING DATE: 10-APR-1989
;SEQ ID NO:9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           망
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APPLICANT: WALLNER, BARBARA

TITLE OF INVENTION: RECOMBINANT DNA

LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN

LINKAGE SIGNAL SEQUENCE

LINKAGE SIGNAL SEQUENCES: 12

CURRENT APPLICATION DATA:
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 Query Match
Best Local Similarity
Matches 266; Conserv
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Best Local Similarity
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FILING DATE: 10-APR-1989
                                                                                           LENGTH: 295
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                  39.98;
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RECOMBINANT DNA MOLECULE COMPRISING
PATATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
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RECOMBINANT DNA MOLECULE COMPRISING
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Score 1363; DB 6;
Pred. No. 2.2e-100;
1; Mismatches 1;
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Pred. No. 9.7e-101;
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1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

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RESULT 53
US-08-284-391B-33
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                                       US-08-284-391B-33
   Query Match
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                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 05-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldem
                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 254 amino acid
                                                                                                                                                                                                                       NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FABUSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEB: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/284,391B FILING DATE: 02-AUG-1994 CLASSIFICATION: 514
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STATE: MA
                                                                                            STRANDEDNESS:
                                                                                                               TYPE: amino acid
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    Application US/08284391B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 Federal Street
                                                                                                                               254 amino acids
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                                                                          linear
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                                                        protein
                                                                                            single
   39.2%;
                                                                                                                                                                                                                                                                  00786/247001
 Score 1338.5;
 DB
 <u>ب</u>
Length 254;
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US-09-218-950-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Seed,
                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED C'
TITLE OF INVENTION: CELLS BY CI
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/OFFILING DATE: 02-AUG-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                             NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: FASTSE(
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                  TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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              LENGTH:
                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
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                                                                                                    617-428-0200
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acid
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Sequence 8, Application US/09313942

Patent No. 6472179

Patent No. 6472179

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILLING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILLING DATE: 1999-09-25
NUMBER: OF SEQ ID NOS: 32
SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 8
LENGTH: 592
TYPE: PRT
CORGANISM: Homo sapiens
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-218-950-33
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Best Local Similarity 98.0%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                     Query Match 37.3%; Score 1275; DB 4; Length 592; Best Local Similarity 47.3%; Pred. No. 5.9e-93; Matches 308; Conservative 53; Mismatches 160; Indels 13
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166 QYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQ---GCGILQPDPPANI 22
                                                                                                        127
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                                                                                                                                          67
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                                                                                                                                                                                                               26 PAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW-------VLRKPA----
                                                                                                                                                                                                                                                 20 PAATQGNKVVLGKKGDTVELTCTASQ-KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                   ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTV 186
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                                                                       PLSN------VVCEWGPRSTPSLTTKA---
                                                                                                                                          -AGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKS 125
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                                                                                                                                                                          RADSRRSLWDQGNFPLIIKNLKIEDSDTYICE-----VBDQKEEVQLLVFGLT 126
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Pred. No. 1.6e-98;
0; Mismatches 0; Indels
                                                                       ----VLLVRKFQNSPAEDFQEPC 165
                                                                                                                                                                                                                                                                                        Indels 130;
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Qy 346NKEAKVSKREKPVWVLNPEAGMWQCLLSDS 375	iS.
Db 246 VERSPHRPILØAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPY 305	브
QY 316 VMRATQLQKNL	<sub>S</sub>
Db 195 FKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDV 245	므
IGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGK	9
Db 167LKNGKE 194	ַם
Qy 203 AFQKASSIVYKKEGEQVEFSFPLAFTVE-KLTGSGELWWQAERASSSKSWITFDLKN-KE 260	iō.
Db 114 FSVNVSDALPSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAV 166	ㅁ
QGGKTLSVSQLELQDSGTWTCTVLQ	iō.
55	מַ
Qy 109 CEVEDQKEEVQLLVFGL-TANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGK 161	g.
Query Match 36.4%; Score 1243; DB 4; Length 622; Best Local Similarity 48.3%; Pred. No. 2.2e-90; Matches 299; Conservative 47; Mismatches 119; Indels 154; Gaps 23;	
; TYPE: PRT ; ORGANISM: Homo sapiens US-09-499-846-2	۲, · ·
SEQ ID NO 2 LENGTH: 622	
CURRENT FILING DATE: 2000- NUMBER OF SEQ ID NOS: 12	
Оян	
APPLICANT: Kavanaugh et al. TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR	
ence 2, nt No. 6	
RESULT 56 US-09-499-846-2	G R
541 PVLDSDGSFFLYSKLTVDKSRWQQGIVFSCSVMHEALHNHYTQKSLSLSPG 591	Д
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Db 481 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 540	дд
515 I	Ş
Db 421 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKT 480	문
455 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAF	٥ و
Db 361 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 420	밁
400 EPKSCDKTHTC	S S
)b 316 TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQDAG 360	밁
2y 344 LENKEAKYSKREKPVWYLNPEAGMWQCLLSDSGQVLLESNIKYLPTWSTPVPCPAP 399	δ.
Db 279 IHDAWSGLRHVVQLRAQEEFGQGEWSEAMGTPW 315	DЬ
284 LPQALPQYAGSGNLTLALEAKTGKLHQEVNLYVMRATQLQKNLTCEVMGPTSPKLML	S
Db 223 TVTAVARNERWISVTWQDEHSWNSSFYRIRFEIRYRAERSKTETTWMVKDLQHHCV 278	밁
239WQAERASSKSW-ITFDL	S

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APPLICANT: Cerretti, Douglas P.
APPLICANT: Borgee, Luis G.
APPLICANT: Borgee, Luis G.
APPLICANT: Fanslow, III, William C.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2900-06-07
PRIOR APPLICATION NUMBER: 60/137,889
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-09-590-656-2
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US-09-590-656-2
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Patent No. 6413932
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                  Matches
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    649
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KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
                                                            IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 570
                                                                                                                                         EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 510
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                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                        PYFGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GQVLLESNIKVLPTWS-TPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKP
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                                                                                                                                                                                                                                                                                                                Score 1237; DB 4; Length 704;
Pred. No. 7.9e-90;
9; Mismatches 12; Indels 3
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RESULT 58 US-09-733-764-2

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GENERAL INC. 0.22.2...
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
APPLICANT: Cerretti, Milliam C.
APPLICANT: Borges, Luis G.
APPLICANT: Borges, Luis G.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/733,764
CURRENT FILLING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/590,656
PRIOR FILLING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-09-733-764-2
                                                                                                                                                                                                                                                         Sequence 6, Application US/09499846
Patent NO. 6656728
GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR IMMUNOGLOBULIN FU
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 6
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                                                                                                                                                                                     LENGTH: 497
TYPE: PRT
CORGANISM: Homo sapiens
US-09-499-846-6
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US-09-499-846-6
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Best Local S
Matches 240
                                                                                                            Query Match 36.2%; Score 1235.5; DB 4; Best Local Similarity 66.2%; Pred. No. 6.3e-90; Matches 255; Conservative 18; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 36.2%; al Similarity 81.4%; 240; Conservative
                                  GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
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                                                                       GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
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 -NKEAKVSKREKPVWVLN---
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Pred. No. 7.9e-90;
9; Mismatches 12
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-PEAGMWQCLLSDSGQVLLESNIK 385
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GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: U5/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEO ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-499-846-4
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Best Local Similarity
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VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                     LFPPKPKDTLM1SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                   ---AWLTVLEALEERPAVMTSPLYLEGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVF
                                                                                                                                                                                                                                                                                  VLPTWST----PVPCPAP-----EPKSCDKTHTC----PELLGGPSVF
                                                                                                                                                                                                                                                                                                                    GSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHS---
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                                                                                  QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                    VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
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                                                   QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                    LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
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                    625
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PCT-US95-03866-12
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
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APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE DOCKET NUMBER: Cy-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CITY: New York
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                            SVMHEALHNHYTQKSLSLSPG
                                                          TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                                                                                      TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                                                                                                                    LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
                                                                                                                                    LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
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Pred. No. 8.6e-90;
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RESULT 63
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Sequence 7, Application US/08157101A Patent No. 5808032 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states exc
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cyto
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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COUNTRY: United States
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Similarity 88.9%;
32; Conservative
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51 Avenue of the Americas
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STRANDEDNESS:
; TOPOLOGY: line
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US-08-157-101A-7
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
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NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9
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APPLICANT: MATSUKURA, SHIGEKAY
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 36.1%; Score 1232.5; DB 1; Similarity 46.7%; Pred. No. 9.7e-90; 7-7-7-2+ive 41; Mismatches 91;
                         CLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPP 424
                                                                                                                                                                                                                                                                        HRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGG-TAALGCL
                                                                                                                                                                                                                                                                                                                                          GNKVVLGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKIL---GNQGSFL--TK 71
                                                                                                QEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQ
                                                                                                                                                                    SWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLH 309
                                                                                                                                                                                                      -----WNSGALASG- 178
                                                                                                                                                                                                                                      QKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSK 249
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MATSUKURA, SHIGEKAZU
TSURUOKA, NOBUO
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPP
                                                                ----NHKPSNTKVDKKV-----
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US-08-397-411-7
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                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-397-411-7
                                                                                                                            Query Match 36.0%; Score 1230.5; DB 3; Length 446; Best Local Similarity 46.7%; Pred. No. 1.3e-89; Matches 284; Conservative 36; Mismatches 103; Indels 185; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08397411
Patent No. 6129914
                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                       TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: line.
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STREET: One reaction
CITY: San Francisco
STATE: California
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tink, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
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                                            LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 70
                                                                                LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
--WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
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RESUL US-08 Seq Pat	Db Q9	Db	\$ 8	B 8	B 8	B 2	? 5	\$ 8	Db :	\$	용 성	뮍	Q	дb
equence 2, Application US/08776511 atent No. 6153190 GENERAL INFORMATION: APPLICANT: Young, Peter R. APPLICANT: Young, Method for Obtaining Receptor Agonist TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 13 CORRESSEE: SmithKline Beecham Corporation- Corporate ADDRESSEE: SmithKline Beecham Corporation- Corporate ADDRESSEE: Patents STREET: 709 Swedeland Road CITY: King of Prussia STATE: Pennsylvania COUNTRY: USA ZIP: 19406-2799 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/776,511 FILING DATE: CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Jervis, Herbert H. REGISTRATION NUMBER: SBC P50349-1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5015	618 KSLSLSPG 625          438 KSLSLSPG 445	78 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS	58 VEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWOOGNVFSCSVMHEALHNHYTO 61	498 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 557	438 VTCVVVDVSHEDPEVKENMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHHODWLNGKE 497 		99	23 QKNILTCEVWGPTSPKIMISIKIENKEAKVSKREKPVWVINPEAGMWQCILISDSGQVILIES 3	66	63 VKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQL 32	203 AFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELMWQAERASSSKSWITFDLKNKEVS 262	114 VSSASTKGPSVFPLAPSSKSTSGG-TAALGCL	SPRO	71 KDTSKNQVSLKLNSLTAADTAVYYCARNDRYAMDYWGQGTLVT 113

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GENERAL INFORMATION:
APPLICANT: KAVANBUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 488
TYPE: PRT
ORGANISM: Homo Bapiens
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US-09-499-846-12
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                                                                                                                                              US-09-499-846-12
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09499846 Patent No. 6656728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                         Matches
                                                                                                        Query Match
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LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                         Similarity
                                   GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE-- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ILE---GRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLDPI 251
GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGRGTEPKSADKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVWVLNPEAGMWQCLLSD-SGQVLLESNIKV-----LPTWSTPVPCPAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TG---KLHQEVNLVVMR-----ATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVKRVTQDPKLQMGKK-------LPLHLTLPQALPQY--AGSGNLTLALEAK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FESKAALLAARGPEEL-----LCFT-ERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOKASSIVYKKEGEOVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITF--DLKNKEV
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                                                                                    35.9%;
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Pred. No. 3.8e
36; Mismatches
                                                                     Score 1225; DB 4;
Pred. No. 4.2e-89;
8; Mismatches 56;
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                                                                                                      Length 488;
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                                                                       49;
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US-08-227-496C-15
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GENERAL INFORMATION:
GENERAL JEFFREY M.
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
TITLE OF INVENTION: Multimeric
TITLE OF INVENTION: Rhinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08227496C Patent No. 6130202
                                                                                                        TELEFAX: (203) 812-54 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           APPLICATION NUMBER: 07/903
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/704
FILING DATE: 05/24/91
APPLICATION NUMBER: 07/556
FILING DATE: 07/20/90
ATTORNEY/AGENT INFORMATION:
                                                                                                                                       REFERENCE/DOCKET NUMBER: MT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
                    MOLECULE TYPE:
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect 8.0 for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Dell OF OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 Morga
   DESCRIPTION:
                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                     LENGTH:
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                                                 : 680 amino acid residues amino acids
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                                                                                                      : (203) 812-5492
(203) 812-5492
TO NO: 15:
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RESULT 68
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                                                                                                                                                                                                                                                                                           Sequence 22, Application Patent No. 5821337
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Best Local Similarity
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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OTHER INFORMATION:
                                                                                        COUNTRY:
                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                               ADDRESSEE:
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                                                                                                              California
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DRMATION: amino acid residues 1-453 =

DRMATION: tICAM(453); amino acid residues 454-680 = amino

DRMATION: acid residues 216-442 of human IgG1 heavy chain
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                                                                                                                                                               Genentech, Inc
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Pred. No. 8.9e-89;
14; Mismatches 114;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 15-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 9070
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000-00194
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US92/05126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,
FILING DATE: 21-Aug-1992
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                      QKSLSLSPG
                                                        OKSISISPG 625
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                                                                                             AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                     -----CNV------NHKPSNTKVDKKV-----
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46.8%; Pred. No. 5.9e-89;
rative 35; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                  EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP
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Indels 179; Length

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US-08-437-642B-22
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Matches
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Patent No. 6054297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/71
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/L
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO
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FILING DATE: 09-May-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San
STATE: Californi
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                                   153
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262 SVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQ 321
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285; Conserv
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                                                                                                                                                                              AVDKSTSTAYMELRSLTSEDSGIYYC------ARWRGLNYGFDVRYFDVWGAGTTV 120
                                                                                                                                                                                                                                                                                      LGKKGDTVELTCTASOKKSIOF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL 86
                                                                                                                                                                                                                                                    LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL
                                                                     LAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEV 261
                                                                                                         TVSSASTKGPSVFPLAPSSKSTSGG-TAALGCL-------
                                                                                                                                           TLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVV 201
                                                                                                                                                                                                                ---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
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46.8%; Pred. No. 5.9e-89;
ative 35; Mismatches 110; Indels 179;
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                                   VKDYFPEPVTVS-----
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                                   WNSGALTSG-
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TELEFAX: 650/>>2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
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US-08-146-206C-22
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                                                                        US-08-146-206C-22
Query Match 35.8%;
Best Local Similarity 46.8%;
Matches 285; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/715272
APPLICATION UNMBER: 14-JUN-1991
ATTOREY/AGENT INFORWATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1 DNA """
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTP 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
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SYSTEM: PC-DOS/MS-DOS
WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5 inch, 1.44 Mb floppy disk
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; Score 1222.5; DB 4;
; Pred. No. 5.9e-89;
35; Mismatches 110;
                                                                                                                                                                                                                                            P0709P1
   Indels 179;
                                    Length
                                    454;
Gaps
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RESULT 71
US-09-705-686-22
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GENERAL INFORMATION:
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ADDRESSEE: Genentech, I
STREET: 1 DNA Way
CITY: South San Francis
STATE: California
COUNTRY: USA
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                  Presta, Leonard G.
TITLE OF INVENTION: Method for Making
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Carter, Paul J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKSLSLSPG
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PCT-US93-07832-22
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  Sequence 22, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0RMATION:
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                                                                                                                                                            QKSLSLSPG
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46.8%; Pred. No. 5.9e-89;
rative 35; Mismatches 110;
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    Immunoglobulin Variants
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/071
FILING DATE: 19930820
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APPLICATION NUMBER:
FILING DATE: 14-JUN-
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: 5.25 inch,
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FILING DATE: 21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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Similarity 46.8%;
                    SNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTP 436
                                                                                                                                                              SVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQ
                                                                                                                                                                                                                                                                                                                                  AVDKSTSTAYMELRSLTSEDSGIYYC-----ARWRGLNYGFDVRYFDVWGAGTTV
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                                                                                             LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE
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460 Point San Bruno
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                                                                                                                                 ----VH-TFPAVL-QSSGLYSLSSVVTVPSSSLGTQTYI-----
                                                                                                                                                                                                 ----VKDYFPEPVTVS-----WNSGALTSG-----
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 -EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP
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US-09-740-002-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Appl
Patent No. 653780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR T
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
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                                                                                                                                                                                                                                                                                           EVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKT 168
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                               AKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTH 408
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                                                                 -QSSGLYSLSSVVTVPSSSLGTQTYI----
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Pred. No. 6.4e-89;
5; Mismatches 111
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   -DKKAEPKSCDKTH
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                                                 US-09-049-672A-4
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GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US, FILING DATE: HEREWITH CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                            IMMEDIATE SOURCE:
LIBRARY: PANCT
CLONE: 1513264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                       NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                              STRANDEDNESS: single
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Score
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1221.5; DB
No. 7.6e-89;
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                                                                                                                                                                                                                                                                                                                                         206 YSLSSVVTVPSSSLGTQTYI-----CNV-----CNV-----NHKPSNTKV
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TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                            TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                        LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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US-08-470-299-4 RESULT 75 Sequence 4, Application US/08470299
Patent No. 5783181
GENERAL INFORMATION: APPLICANT:
APPLICANT: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA: APPLICANT: APPLICANT: Shatzman, AlTITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline STREET: COUNTRY: 19406 F: 709 Swedeland King of Prussia Pennsylvania USA Chapman, Conrad Clinkenbeard, H Young, Peter R. Murphy, Browne, Kay E. Michael J. Conrad G. Allan R. No. 5783181el Compounds Beecham Corporation Road, P.O. Box 1539 Helen H Version #1.30

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APPLICANT: COSMAN, David J.
APPLICANT: MULLBERG, JUEGEN H.
APPLICANT: MULLBERG, JUEGEN H.
APPLICANT: MUSLOW III, William C.
APPLICANT: KUBIN, MARZEK
TITLE OF INVENTION: ULBP DNA AND POLYPEPTIDES
FILE REFERENCE: 2866-USA
CURRENT APPLICATION NUMBER: US/09/532,856
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: PCT/US98/27048
EARLIER FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: 60/069,857
EARLIER APPLICATION NUMBER: 60/092,946
EARLIER APPLICATION NUMBER: 60/092,946
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 10
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US-09-532-856-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09532856
Patent No. 6458350
GENERAL INFORMATION:
LENGTH: 453

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(223)
OTHER INFORMATION: ULBP-2 sequences
                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.7%; Score 1220.5; DB 1; Length 387; Best Local Similarity 83.4%; Pred. No. 6.8e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SULLON, Jeffrey A.
REFERENCE/JOCKET NUMBER: 34,028
REFERENCE/JOCKET NUMBER: 93109C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-59024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 VSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPT--WSTPVPCPA-PEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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                                                                                                                                                                                           TITLE OF INVENTION: ULBP DNA AND POLYPEPTIDES
FILE REFERENCE: 2866-US
CURRENT APPLICATION NUMBER: US/09/524,100C
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: PCT/US98/27048
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 60/069,857
PRIOR APPLICATION NUMBER: US 60/069,857
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/092,946
PRIOR APPLICATION NUMBER: US 60/092,946
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-524-100C-6
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; LOCATION: (224)...(453)
; OTHER INFORMATION: Human Ig Fc
US-09-532-856-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 6, Application US/09524100C
; Patent No. 6653447
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: COSMAN, David J.
APPLICANT: MULLBERG, Jurgen H.
APPLICANT: FANSLOW III, William
APPLICANT: KUBIN, Marek
APPLICANT: KUBIN, Marek
                                                                                                                                   SEQ ID NO 6
LENGTH: 453
TYPE: PRT
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Best Local (
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FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(223)
                                                                  FEATURE:
OTHER INFORMATION: Peptide
                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 HEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GPRWCAVQGQVDEKTFLHYDCGNKTVT-----PVSPLGKKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 35.7%; Score 1220.5; DB Similarity 58.9%; Pred. No. 8.6e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOVLLESNIKVLPTWSTPVPCPAPEP---KSCDKTHTC----PELLGGPSVFLFPPKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MULLBERG, Jurgen H. FANSLOW III, William C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGDCIGWLED- 196
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TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU.
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 497
TYPE: PRT
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US-09-499-846-10
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                                                                                                        Query Match
Best Local S
Matches 253
                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09499846
Patent No. 6656728
GENERAL INFORMATION:
APPLICANT: Kavanaugh et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
LOCATION: (224)..(453)
OTHER INFORMATION: Human
-09-524-100C-6
                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: ULBP-2 sequences
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Local Similarity 58.9%;
les 258; Conservative 3
                                                                                                           Local Similarity
les 253; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQVLLESNIKVLPTWSTPVPCPAPEP----KSCDKTHTC-----PELLGGPSVFLFPPKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVTTAWKAQNPVLREVVDIL----TEQLRDIQLENYTPKEPLTLQARMSCEQKAEGHSSG
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                                               GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
                                                                          GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEALHNHYTOKSLSLSPG
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                                                                                                        35.7%;
ilarity 65.7%;
Conservative 1
--NKEAKVSKREKPVWVLN-----PEAGMWQCLLSDSGQVLLESNIK 385
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                                                                                                        Score 1220.5; DB 4;
Pred. No. 9.8e-89;
.8; Mismatches 56;
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Pred. No. 8.6e-89;
1; Mismatches 70;
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GENERAL INFORMATION:

APPLICANT: KAVANAION:
FIED OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOTTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
SEQ ID NOS 12
ORGANISM: Homo Sapiens
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US-09-499-846-8
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Best Local Similarity
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                                                                                                                                                                                                                         263 ---AWLTVLEALEERPAVMTSPLYLEGSGSPGLOEPKSCOKTHTCPPCPAPELEGGPSVF
                                                                                                                                                                                                                                                         386 VLPTWST--
                                                                                                                                                                                                                                                                                      206 GSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHS---
                                                                                                                                                                                                                                                                                                                                               146 GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
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                                                                                                                        VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                           GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
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                                       QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                            LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYNSTYR
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VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                     VVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                 -----PEAGMWQCLLSDSGQVLLESNIK 385
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                                                                                                                                                                                                                                                  -PVPCPAP-----EPKSCDKTHTC-----PELLGGPSVF
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pred. No. 1.1e-88;
8; Mismatches 56;
            625
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VFSCSVMHEALHNHYTOKSLSLSPG

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RESULT 81
US-09-301-593-18
(Sequence 18, Application US/09301593A
Patent No. 6455677
(GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Leger, Olivier
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
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APPLICANT: Bevilacqua, Michael P.
APPLICANT: Golling, David S.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR
TITLE OF INVENTION: DISEASES
FILE REFERENCE: A-365F
CURRENT APPLICATION NUMBER: US/09/131,247
CURRENT APPLICATION NUMBER: 05/055,185
EARLIER APPLICATION NUMBER: 60/055,185
EARLIER APPLICATION NUMBER: PCT/US 97/02131
EARLIER APPLICATION NUMBER: PCT/US 97/02131
EARLIER FILING DATE: 1997-02-10
NUMBER: OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-09-131-247-16
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SEQ ID NO 16
LENGTH: 388
TYPE: PRT
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEA--GMWQC 370
                                                                                                                                                                                                                                                                                              GNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFLFPEKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAMEADOPVSLTN---MPDEGVMVTKFYFQEDEAAAEPKSSDKTHTCPPCPAPELLGGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFYLRNNQL-VAGYLQGPNVNLEEKIDVVPIEPHALFLGIHGGKMCLSC-VKSGD-ETRL 79
                                                                                                                                                                                                                                                                          GNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                           YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
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65.9%;
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Pred. No. 7.5e-89;
3; Mismatches 73;
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; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 18
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                         RESULT 82
US-09-740-002-27
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Sequence 27, Application US/09740002
Patent No. 6537809
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: BUTTRALIZING HI
TITLE OF INVENTION: SPECIFIC TO RS
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                                                                                                                                                                                                                  QKSLSLSPG
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46.1%; Pred. No: 1e-88;
vative 42; Mismatches 107;
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 HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES RSV F-PROTEIN AND METHODS FOR THEIR
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; Sequence 12, Application U
; Patent No. 6113898
; GENERAL INFORMATION:
APPLICANT: Anderson, D
; TITLE OF INVENTION: "M
; TITLE OF INVENTION: TO
                                                                                                RESULT 83
US-08-487-550-12
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LENGTH: 475
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Best Local :
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CURRENT APPLICATION NUMBER: 09/9/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.1
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED F
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Pred. No. 1.1e-88;
1; Mismatches 116;
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Best Local Similarity 53.7%;
Matches 277; Conservative 3:
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ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PHITITLE OF INVENTION: IMPORTANT OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
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STREET: 69
CITY: Alex
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TOPOLOGY: linear
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TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                       TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                   LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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                                                                                                                                                                                                                                                                                                                                                                                                             -NSMTAADTAVYYCVRDRLFSVVGMVY-----NNWFDVWGPGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1219.5; DB 3;
Pred. No. 1.1e-88;
1; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version
                                                                                                                                                                                                                                                                                                         -NIKVLPTWSTPVPCPAPEPKSCDKTHTC----
                               625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SGGSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMENT TO3-B36-2021
TELEPAX: 703-B36-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 84
US-09-526-098-12
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.7%;
Best Local Similarity 53.7%;
Matches 277; Conservative 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107070707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                    142
                                                                                                                              334
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                                                                                                                                                                                                       281 HLTLPQALPQYAGSGNLTLALEA----KTGKLHQEVNLVVMRATQLQKNLTCEVWGP--- 333
                                                                                                                                                                                                                                                                                                                                                                               171 VSQLELQDSG------TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVE 220
202 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS-NTKVDKKA-EPKSCDKTHTCPPCP 259
                                                                                                                                                                                                                                                                                             221 FSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL 280
                                                                                                                                                                                                                                                                                                                                           18
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                                                                                                                                                                                                                                                     GGYGWGW-IRQPPGKGLEWIGSFYSSSGNTYYNPSLKS-QVTIS--TDTSKNQFSLKL-- 103
                                                                                                                                                                                                                                                                                                                                           LSQVQLQESGPGLVKPSETLSLTCAV------
                                       LLSDSGQVLLES-------AIKVLPTWSTPVPCPAPEPKSCDKTHTC---- 410
                                                                                 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 201
                                                                                                                         -----TSPKLMLSLKLENKEAKVSKR------EKPVWV-----LNPEAGMWQC 370
                                                                                                                                                                   -----NNWFDVWGPGVL 141
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PHONKEY MONOCLONAL ANTIBODIES SPECIFIC

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MONTAINING, AND USE THEREOF AS

ENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1219.5; DB 4;
Pred. No. 1.1e-88;
1; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Qy 426 PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 485	
Db 187 VLQSSGLYSLSSVVTVPSSSDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 241	
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Query Match 35.6%; Score 1216; DB 4; Length 442; Best Local Similarity 89.6%; Pred. No. 1.9e-88; Matches 233; Conservative 3; Mismatches 14; Indels 10; Gaps 2;	
, NOLECULE TYPE: protein US-08-472-888A-7	
STRANDEDNESS: unknown	
; LENGTH: 442 amino acids ; TYPE: amino acid	
; INFORMATION FOR SEQ ID NO: 7: ; SEQUENCE CHARACTERISTICS:	
; TELEFAX: 617-428-7045 ; TELEX:	
REGISTRATION NUMBER: 35,238 REFERENCE/DOCKET NUMBER: 00786/258001	
; ATTORNEY/AGENT INFORMATION: ; NAME: Elbing Karen L	
; APPLICATION NUMBER: 07/618,314 . ; FILING DATE: 23-NOV-1990	
FILING DATE: 03/07/1/2/000H	
TA:	
; OPERATING SYSTEM: DOS ; SOFTWARE: FastSEQ for Windows Version 2.0	
IBM Com	
COMPUTER READABLE FORM:	
; COUNTRY: USA ; ZIP: 02110	
₽à	
176 Federal Street	
ADDRESS	
EQUENCES: 9	
TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS	
; APPLICANT: Seed, Brian : APPLICANT: Walz, Gerd	
o. 6613746 INFORMATION:	
ULT 85 08-472- equence	
Db 440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475	
QY 590 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625	
Db 380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 439	
Qy 530 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 589	
Db 320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379	
QY 470 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 529	
Db 260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 319	
QY 411 -PELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 469	

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PCT-US96-10043-9
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GENERAL INFORMATION:
APPLICANT: The General Hospital C
                                                                                                                                                                                    Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COFFRATING SYSTEM: PC-DOS/MS-DOS
COFFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Lech, Karen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14-JUN-:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                         Local 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/10043 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                    187
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                                 242
                                                                   426
486
                                                                                                                                    371 LLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPK 425
                                                                                                                                                                                     Similarity
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TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 545
                                                                                                    VLQSSGLYSLSSVVTVPSSSDKKV-----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPK
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                                                 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
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                               PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
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                                                                                                                                                                                                                                                                                                                                                                                           617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The General Hospital Corporation VENTION: P-SELECTIN LIGANDS AND
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                        not relevant
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89.6%;
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                                                                                                                                                                                    Score 1216; DB 5;
Pred. No. 1.9e-88;
                                                                                                                                                                     ed. No. 1.9e-88;
Mismatches 14
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                                                                                                                                                                                                       Length 442;
                                                                                                                                                                       Indels
                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                    PCT-US96-10043-11
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 14-UN-1995
CLASSIFICIATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02210-2804
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617/542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT
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                                                                                                                                                       397 PAPEPKSCDKTHTC-----PELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPE
323
                                                                263 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                   452 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                  203 PEGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                    227;
                                                                                                                                                                                                                                                                                                                                      amino acid
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 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
                   EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 571
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                                                                                                                                                                                                                                                                                                                                                    437 amino acids
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         617/542-5070
                                                                                                                                                                                                                                                                                                                   not relevant
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Pred. No. 2e-88;
O; Mismatches
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RESULT 89
US-09-157-452B-12
; Sequence 12, Application US/09157452B
; Patent No. 6482409
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US-08-378-939-10
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GENERAL INFORMATION:
GENERAL INFORMATION: JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
APPLICANT: LEWIS, PRODUCTION OF ANTIBODIES
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APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                          35.6%;
Local Similarity 97.8%;
les 226; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                   EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
                                                                                                                                                                                               ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 574
                                                                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                          ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                        PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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555 THIRTEENTH ST. N.W.
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Pred. No. 2.5e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 476;
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APPLICANT: Lobb, Roy R.
APPLICANT: Burkly, Linda C.
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
CURRENT APPLICATION NUMBER: US/09/157,452B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR FILING DATE: 1997-10-15
PRIOR APPLICATION NUMBER: US 08/373,857
PRIOR APPLICATION NUMBER: US 08/373,857
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR APPLICATION NUMBER: US 07/835,139
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR APPLICATION NUMBER: US 07/835,139
PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 TANSDTHLLO-GQSLTLTLESPPGSSP----SVQCRSP-RGKNIQGG--KTLSVSQLELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 NEHSYLCTATCESRKLE-------KGIQVEIYSFP------
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                                                                                                                                                                                  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                               LTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                         VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                         PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                             REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
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                                                                             PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                                                                             PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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52.4%; Pred. No. 3e-88;
tive 40; Mismatches
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  445
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; Sequence 13, Application
; Patent No. 5777085
; GENERAL INFORMATION:
APPLICANT: Co, Man St
APPLICANT: Tso, J. Yu

US/08458516

Co, Man Tso, J.

RESULT 90 US-08-458-516-13

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RESULT 91
US-09-485-737B-67
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                                                                                                                                                              Sequence 67, Application US/09485737B Patent No. 6350860 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
FILE REFERENCE: INNS:015
CURRENT FAPPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT EP 98/05165
PRIOR FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/059
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: William M. Smith STREET: One Market Plaza, St CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                             575
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Pred. No. 3.3e-88;
0; Mismatches 0;
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RESULT 92
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 67
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Best Local Similarity
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PRIOR TILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 468
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                              DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                     EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLP
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                                                                                                                        PSREEMTKNOVSLITCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
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45.3%;
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Pred. No. 3.96
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GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

REFERENCE: INNS:015

Sequence 90, Application US/09485737B Patent No. 6350860

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CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
SOPTWARE: PATENTIN VERBION 3.0
SEQ ID NO 90
LENGTH: 711
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                                                                              RESULT 93
US-09-313-942-7
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Sequence 7, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS,
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Best Local
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Local Similarity 45.3%;
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                                                                                                                                                       DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI TITLE OF INVENTION: AND USING FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                             APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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                                                                                                                                ; TYPE: PRT; ORGANISM: Homo US-09-313-942-9
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US-09-313-942-9
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                                                                Query Match
Best Local Sin
Matches 226;
                                                                 Matches
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Best Local Similarity
Matches 229; Conserv
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                                                              Score 1212.5; DB 4; Pred. No. 1.1e-87; 0; Mismatches 0;
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Pred. No. 9.3e-88;
3; Mismatches 5;
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US-09-247-352-3
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APPLICANT: Siadak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgen
APPLICANT: Huse, William D.
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TYPE: PRT
ORGANISM: Human and
09-247-352-3
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TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN
FILE REFERENCE: DB2a SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
MUMBER: OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
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 VLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMI 432
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                                                                 RATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQ 377
                                                                                                                    NKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVM
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US-09-466-635-3
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Best Local Similarity 46.7%;
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GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Siadak, Anthony W.
APPLICANT: Siadak, Anthony W.
APPLICANT: Harris, Linda
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgen
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD4
FILE REFERENCE: DB2 SEQUENCE
CURRENT PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 451
TYPE: PRT
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                                                                                    378 VLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMI 432
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SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 492
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GENERAL INFORMATION:

APPLICANT: Park, John E.

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Leger, Olivier

APPLICANT: Leger, Olivier

APPLICANT: Saldanha, Jose W.

FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A

CURRENT APPLICATION NUMBER: EP 98107925.4

EARLIER APPLICATION NUMBER: US 60/086,049

EARLIER APPLICATION NUMBER: US 60/086,049

EARLIER APPLICATION DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

COLTENBRE: DATE: 1998-05-18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-30
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US-09-301-593-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 30
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Patent No. 6455677
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HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
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                                                                                                                                                                           GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWS
                                                                                                                                                                                                                CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV-
                                                                                                                                                                                                                                                    LTLPQALPQYA----GSGNLTLALEA-----KTGKLHQEVNLVVMRATQL-QKNLTCEVW 331
                                                                                                                                                                                                                                                                                                                            SFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLH 281
                                                                                                                                                                                                                                                                                                                                                                                                          KTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSSPSVQCRSPR------GKNIQG-----
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                                                                                                                                       ------NHKPSNTKVDKKV------ 240
                                                                                                                                                                                                                                                                                                                                                                      KSSSTAYMELRSLTSEDSAVYFCA----RRRIAYGYD------EGHAMDY
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                                                           - EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 472;
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US-08-595-043A-50
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Best Local Similarity 97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SGARLATO,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION UNMER: 32,837
REFERENCE/DOCKET NUMBER: SGAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353
                                                                                                  515 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 574
                                                                                                                                                                                                                                                      400 EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
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                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                          ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                          Score 1211.5; DB 2;
Pred. No. 1.7e-88;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAR-00371
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  231
                                        625
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RESULT 99 US-09-178-869-2

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APPLICANT: Wong, Shou
APPLICANT: Wong, Shou
APPLICANT: Horney, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERNCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
SEQ ID NO
SEQ ID NO
CRGANISM: Homo sapiens
US-09-761-413-2
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Patent No. 6197294

GENERAL INFORMATION:
APPLICANT: Tao, Weng
APPLICANT: Hong, Shou
APPLICANT: Hammang, Joseph P.
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward

TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043

CURRENT APPLICATION NUMBER: US/09/178,869B

CURRENT FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
LENGTH: 331
Type: PRT
ORGANISM: Homo sapiens
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US-09-761-413-2
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Patent No. 6506891
GENERAL INFORMATION:
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Best Local Similarity 97.8%;
Matches 226; Conservative
                                                                                  Query Match
Best Local Similarity
Matches 226; Conserv
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                    400 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
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100 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
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      515
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      ISKAKGQPREPQVYTLPDSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
      279

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      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
      625

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      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Search completed: August 3, 2004, 13:17:11 Job time: 29.0695 secs

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N-PSDB; AAN90357.
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diagnosis; CD4;
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02-NOV-1992
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                                       The fusion protein
                                                               Example;
                                                                                                                                                                                                                    22-JAN-1988;
                                                                                                                                                                                                                                                                    26-JUL-1989
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                      Immunoglobulin-CD4 fusion proteins infections or detecting HIV or SIV
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                                                             Table 2, Page
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                                                                                                                                                                                                                                                                                                                                            immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable region
genes of the invention pref. comprise cDNA sequences ra fragment which binds gp120 ligated to an expression des an antibody in which the variable region of the ted (see WO87-02671). The CD4 portion of the fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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Glu (17)

Asn (72)

Asn (88)

Leu (127)

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Tle (23)

Asp (155)

Gly (48)

His (132)

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Human CD4

Ser (121)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The Igheavy chain is pref: from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Pmu, CD4E-gamma1, and CD4Mmu (No. 67608), pCD4P-gamma (No. 67609) and pCD4E-gamma-1 (No. 67610). The plasmid containing (pCD4E-gamma-1) has been deposited in E. coli (MC1061/P3) at the ATCC under accession number 67610. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 631 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                            WOOGNVFSCSVMHEALHNHYTOKSLSLSPG
                                                                          ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                    NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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AAB19508 standard; AAB19508; protein; 631 ₽

09-JAN-2001 (first entry)

CD4-IgG1 fusion protein CH4Egammal

gp120; CD4; IgG1; human; CD4Egamma1; fusion therapy; diagnosis. protein; immunoglobulin; HIV; SIV;

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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of fusion protein CD4Egammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its Cterminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge region (see AAA50661). Fusion protein CD4Egammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Egammal provide both complement-mediated and cell-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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)B; AAA50661.
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                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                   QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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89US-00299596.
92US-00896781.
93US-00057952.
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Pred. No. 3e-166;
0; Mismatches
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This invention describes a novel nucleic acid (I) encoding a fusi protein comprising a DNA sequence encoding amino acids 1-173 of C and a DNA sequence encoding a human immunoglobulin (Ig) heavy or chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding gp120. The fusion protein is useful for treating human immunodeficiency virus (SIV). This sequence virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from linked to human IgG1 upstream of the hinge region

human immunodeficiency

1). This sequence

from CD4

fusion of CD4

(II)

or light

Example

1; Col

29-42;

39pp; English

Sequence 631

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23-JAN-1989;
09-JUN-1992;
                                                                                                                Fusion protein useful
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                                                                                                                                                                                                                                                   21-DEC-1999.
                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                    Synthetic
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89US-00299596.
92US-00896781.
93US-00057952.
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Best Local S
Matches 619
                                                                   CA1340741-C
                                                                                                                        HIV; extracellular; CD4; gp120; immunoglobulin; Ig; secreted protein; SIV infection; medicament.
                                                                                                                                                                               14-MAR-2000
                                                                                                                                                                                                                          AAY59169
  20-JAN-1989;
                       20-JAN-1989;
                                           14-SEP-1999
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Pred. No. 3e-166;
0; Mismatches
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PA (GEHO) GEN HOSPITAL CORP.

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PI Seed B;

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WPI; 2000-063015/06.

DR N-PSDB; AAZ48202.

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New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in PT the treatment of HIV or simian immunodeficiency virus infections.

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PT New fusion gene encoding immunoglobulin-CD4 fusion protein that CCC comprises an extracellular CD4 DNA sequence or its fragment which binds CCC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA CCC sequence of an Ig heavy or light chain, where the DNA sequence encoding CCC the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is CCC capable of being secreted. The fusion proteins are useful for treating CCC infections in humans in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CCC infections in humans. The present sequence represents the fusion protein of the hinge region

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Sequence 631 AA;

Query Match

94.6%; Score 3229.5; DB 3; Length 631;
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ģ ૈ 8 g, S S 밁 밁 Ś 밁 Ś Ś g á 밁 á 문 Ś 문 밁 Query Match Best Local S .Matches 619 301 476 421 361 361 181 181 121 121 al Similarity 619; Conserv 5 62 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLG LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL Conservative 94.6%; Score 3229.5; DB Pred. No. 3e-166; 0; Mismatches 6 ٠<u>.</u> Indels <u>ح</u> Gaps 420 415 360 360 300 240 120 60 595 540 535 480 475 300 240 180 180 120 600

WQQGNVFSCSVMHEALHNHYTQKSLSLSPG

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Best Local S
Matches 621
                                                                                                                                                                                                                                                            The fusion protein genes of the invention pref. comprise cDNA sequences which encode CD4 or a fragment which binds gpl20 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see W087-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The Ig heavy chain is pref. from IgM, IgG1 or IgG3 The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Pmu, CD4E-gamma1, and CD4Mmu (NO.67608), pCD4P-gamma (No.67609) and pCD4E-gamma1.

(No.67610) The plasmid containing (pCD4H-gamma-1) has been deposited in E. coli (MC1061/P3) at the ATCC under accession number 67611. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic construct which encodes site upstream of the CH1 region
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-214472/30.
N-PSDB; AAN90356.
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02-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin-CD4 fusion proteins - used for treating infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-1989;
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                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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gp120; binding fragment; glycoprotein; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 12-23; 68pp;
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Pred. No. 2.5e-1
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protein CD4H-gamma-1).
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les 4;
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                                                  VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                            VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                     YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
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AAB19507 standard; protein; 729 3

AAB19507;

CD4-IgG1 fusion protein CH4Hgammal.

09-JAN-2001

(first

entry)

CD4; Ig gp120; IgG1; human; CD4Hgamm
0; therapy; diagnosis. CD4Hgamma1; fusion protein; immunoglobulin; HIV;

Homo sapiens.

RESULT 6
AAB19507
ID AAB1
XX AAB1
XX CD4XX CD4XX CD4XX CD4XX YD12
XX Y 23-JAN-1989; 09-JUN-1992; 12-APR-1993; 07-JUN-1995; US6117656-A. 04-FEB-1994 22-JAN-1988 12-SEP-2000 Protein Protein 88US-00147351. 89US-00299596. 92US-00896781. 93US-00057952. 94US-00191708. 95US-00479353 400. Location/Qualifiers /note= "CD4 extracellular region" note= .729 .e= "IgG1 heavy chain"

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Query Match
Best Local S
Matches 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of fusion protein CD4Hgammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the CH1 region (see AAA50660). Fusion protein CD4Hgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Hgammal provide both complement-mediated and cell-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; AAA50660.
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YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                       TAALGCLVVSYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
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                                            VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                         VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                            ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                                                                                                                                                                                                                                                                                                                             LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                         -EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPE
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Pred. No. 2.5e-163;
0; Mismatches 4;
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                         Query Match
                                                                               The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections. The present sequence represents the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; extracellular; CD4; gp120; immunoglobulin; Ig; secreted protein; SIV infection; medicament.
                                                Sequence 729
                                                                                                                                                                                                                                                         New fusion gen
the treatment
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                                                                                                                                                                                                                                 Example 1;
                                                                       upstream of the CH1
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661 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
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                                                                                                                                                                                                                                                         gene encoding immunoglobulin-CD4 fusion proteins, use
ent of HIV or simian immunodeficiency virus infections
 93.0%;
ilarity 85.3%;
Conservative
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                       Fusion protein; anti-human immu
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Synthetic.
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92US-00896781.
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                YKCKVSNKALPAPI
                                                              VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
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                                               VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                            ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPE
                                                                                                                                      TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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nilarity 85.2%;
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                | EKTISKAKGQPRBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
   EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                          EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPE
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Pred. No. 8.8e-163;
0; Mismatches 5;
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD45gammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 616 AA;
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                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                 WPI; 2000-063015/06.
N-PSDB; AAZ48205.
                                                                                                                                                        New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in the treatment of HIV or simian immunodeficiency virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which b to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Bgammal where the CD4 is linked to human IgG1 at the Banl site
                             Genetic
                 downstream
                                                                                                                               AAP93012
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              construct which encodes CD4 linked to human IgG1 at eam from the hinge region (fusion protein CD4Blambda
                                                                                                                               standard;
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Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy; diagnosis; CD4; gp120; binding fragment; glycoprotein; variable
sapiens
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Seed 26-JUL-1989 (GEHO) 22-JAN-1988; 20-JAN-1989; 1989-214472/30. )B; AAN90360. GEN HOSPITAL 88US-00147351 89EP-00100913 CORP

Immunoglobulin-CD4 fusion proteins - used for infections or detecting HIV or SIV in sample. treating g

Example; Table 5, Page 48-55; 68pp; English.

The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see Wo87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The 19 heavy chain is pref. from 19M, IGG1 or IGG3. The following are specifically claimed: fusion proteins CD4H1ambda1, CD4Mmu, CD4Pmu, CD4Elambda1, and CD4Mmu (No. 67608), pCD4Plambda (No. 67609) and pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)

Sequence 614 ξ

606;

Conservative

Similarity

91.7**%**; 97.0**%**;

Length

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                                                       LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
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                                           LNPEAGMWQCLLSDSAQVLLESN:
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Pred. No. 5.3e-161;
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                                           The present sequence is that of fusion protein CD4Bgammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Ban1 site downstream of the hinge region (see AAA50664). Fusion protein CD4Bgammal and a nucleic acid, end a method of producing the fusion protein to comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NRT imaging agent. The fusion protein the fusion protein or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion protein such as CD4Bgammal provide both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-1992;
12-APR-1993;
04-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD4-immunoglobulin fusion proteins, useful for targeting
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23-JAN-1989;
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94US-00191708.
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89US-00299596
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                             cell-mediated
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ARRESULT 13
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                                            Region
                                                                                                                                                                      25-MAR-2003
28-JAN-1993
Region
                      Region
                                                                                  Synthetic.
                                                                                                          therapy; diagnostic
                                                                                                                       CD4-gamma
                                                                                                                                                                                                            AAR26531;
                                                                                                                                                                                                                                  AAR26531 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                           VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFPFKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVFGLTANSDTHILLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                              VESCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                   VFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                              QVSLTCLVKCFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                                                                                                                                                           QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                        chimeric heavy
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                                                                                                                                                CD4-IgG1
                                                                                                                                                                      (revised)
(first en
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/label= CH1
303. .317
/label= hinge
318. .427
                                  205. .30
/label=
                                                           Location/Qualifiers
                                                                                                                                                                                                                                  protein;
                                                                                                         c heavy chaim homodimer; agent; inhibition.
                                                                                                                                                                       entry)
                                                                                                                                                chimeric
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Pred. No. 1e
                                                                                                                                               heavy chain heterotetramer.
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1e-157;
                                                                                                                       expression vector; HIV;
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Best Local Similarity
Matches 457; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into M13mp18. In order to excise a fragment containing the CH1 exon of the human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mp18 (CD4) vector. Oligonucleoride-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-IgG1HC-pRcCMV (ATCC 75192). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 4; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -for preventing and treating HIV infection useful as a diagnostic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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DB; AAQ27831.
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                ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL
                                                                                                                                                                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFFLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                               TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK 356
                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAF--AST-----KGPSV---FPL------
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                                                                                  PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----P
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428. .534
/label= CH
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72.1%;
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Pred. No. 1
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..9e-111;
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                                                                                          CD4-gamma 1 chimeric heavy chain homo-dimer and its for preventing and treating HIV infection useful as
                                                                                                                                                              08-FEB-1991;
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28-JAN-1993
                                                                                                                                   Beaudry
                                                                                                                                                (PROG-) PROGENICS PHARM INC
                                                                                                                                                                           10-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic
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                                                                                                                                                                                                                                                                                                                             one
                                                                                                                                                                                                                                                                                                              chimeric heavy
                                                                                                                                   Maddon
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(first entry)
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                                                                                                                                                                                                                                                                                                                           chain of a CD4-gamma 1 chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                         /label= C
/note= "1
                                                                                                                                                                                                                               220. .329
/label= CH2
                                                                                                                                                                                                                   /label= CH3
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                            label= hinge
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                                                                                                                                                                                                                                                                                                        agent;
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                                                                                          expression vector a diagnostic agent
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Human CD4 cDNA was excised from pSP6T4 and cloned into Ml3mpl8. The 2 kb PstI/PstI fragment from pBR lambda 1 contg. the human lambda 1 heavy chain gene (contg. the hinge, Ch2 and CH3 exons) was isolated and cloned into the BAP-treated Ml3mpl8/CD4 vector. To obtain a CD4-lambda 1 chimeric heavy chain gene, oligonucleotide-mediated site-directed mutagenesis was performed to juxtapose the CD4 and lambda 1 heavy chain DNA sequences, ligating the CD4 sequence in frame to the hinge exon. The DNA was then cloned into pcDNA-1 to produce CD4-IgG1-pcDNA1 (ATCC 40951) (Updated on 25-MAR-2003 to correct PN field.)

cloned Š Example; Fig

3; 88pp; English.

Sequence 435

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RESULT 15
AAR26783
ID AAR26
XX AAR26
XX AAR26
DT 24-OC
DT 25-MA
DT 06-FE
XX CD1-I
CDE CD4-I
XW homod
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FT Domai
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Best Local S
Matches 428
                                                                                                                                                                                        24-OCT-2003
25-MAR-2003
                                                                                                                    chimeric;
                                                                                                                                                      CD4-IgG2
                                                                                                                                                                                                                                                   AAR26783 standard; protein; 530
                        Domain
                                                                                           Homo sapiens
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                                                                                                                                                      chimeric heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL
                                                                                                                                                                                                                                                                                                                          QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT
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                                                                                                                                                                                                                                                                                                                                                           LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                       LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                        STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTCTVLQNQKKVEFKIDIVVLAF------
                                                                                                                                                                                                                                                                                                             QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                    increased
                                                                                                                               soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                           (revised)
(revised)
(first entry)
/label= CD4 domain
206. .302
/label= CH1 domain
303 .312
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EPKSCDKTHTCPPCPAPELLGG
                                                                                                                  CD4; T
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Pred. No. 1.2e-107;
0; Mismatches 1;
                                                                                                                    receptor;
life; HIV
                                                                                                                                                                                                                                                                                                                                   625
                                                                                                                                                                                                                                                                                                             434
                                                                                                                    CD4 antigen; high recovery; infection; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer It was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exortoxin A (domains) I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors treatment, prevention and diagnosis of HIV infection.
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      357
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                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
437; Conserv
                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                           61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                        MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                           MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
        PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
                                                                                                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL
                                                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                         TFPAVLOSSGLYSLSSVVTVPSSNFGTQTYTCNV
                                                                      TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CH7
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                                                                                                          ----PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2116; D
Pred. No. 2.8e
25; Mismatches
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.8e-106;
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Gaps

240

297 216 180 120 120 60

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This sequence represents the CD4-IgG2 chimeric heavy chain amino acid consequence from the CD4-IgG2 chimeric heterotetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a cytotoxic to an immunoconjugate comprising a cytotoxic radionuclide and a cytotoxic radionuclide is linked to either the heavy chains or the light chains, or cadionuclide is linked to either the heavy chains or the light chains, or consider the comprision of the light chains, or consider the consequence of the light chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by cector CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa chains encoded by vector CD4-Kappa chains encoded on the CD4-igg2HC-pRcCMV (ATCC 75193) and both light chains are chimeric consequence of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex conditions of the surface of antigen presenting cells to complex conditions. In humans CD4 is conditionable of interactions in humans CD4 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .07-AUG-1992;
06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
                                                                                                                                                                                                                                                                                                                                        New immunoconjugate, used to treat, prevent or deficiency virus infection, comprises radionuc heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allaway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
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93WO-US007422.
95US-00379516.
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RESULT 17
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DT 23-AE
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DE CD4-1

standard;

protein;

AAB67323 st AAB67323; 23-APR-2001

(first entry)

CD4-IgG2 chimeric heavy chain

protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                       PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTV
                                                                                                                                       EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                                                                                                                                                                                                                                                            P-----SNTKVDKTVERKCCVECPPCPAPP---
                                                                                                                                                                                                                                                                                                             PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
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25; Mismatches
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Matches 437
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2HC-pReCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kLC-pReMV. The invention is useful for killing human immunodeficiency virus (HTV)-infected cells, for the treatment and prevention of infection with HTV
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kappalight
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ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                                                                                                                                                                                                            TWTCTVLQNQXKVEFKIDIVVLAF--AST-----KGPSV---FPLA------
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                                                                      PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----
                                                                                                   TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV-
                                                                                                                            TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
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93WO-US007422.
95US-00379516.
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                                                                                                                                                         --PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2116; DB 4;
Pred. No. 2.8e-106;
5; Mismatches 58;
                                           SNTKVDKTVERKCCVECPPCPAPP
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10-FEB-1992;
08-DEC-1992;
                                   The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgC2HC-PRCCMV (VI) and CD4-KLC-PRCCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+cells infected with HIV. The prevent CD4-IgG2 chimeric heterotetramer. This sequence was used in the
                                                                                                                                                                                                                                                           Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ or treating a subject having CD4+ cells infected with HIV involves CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
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                                                                                                                                                                                                                                  Disclosure; Fig
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92WO-US001143.
92US-00960440.
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Matches

Query Match Best Local Similarity

62.0%;

Score 2116; DI Pred. No. 2.8e 25; Mismatches

e 2116; UB -, 1. No. 2.8e-106; 1. No. 58;

Length 530; Indels

114;

10;

Sequence

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Synthetic.
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 07-JUN-1995;
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                           17-SEP-2002.
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                                                                                          Protein
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                                                                                                                                                                                                           CD4; immunoglobulin
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26. .530
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                                                                              chimeric heterotetramer"
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SQ Sequence 530 AA;

Query Match
62.0%; Score 2116; DB 6; Length 530;

Best Local Similarity 68.9%; Pred. No. 2.8e-106;

Best Local Similarity 68.9%; Pred. No. 2.8e-106;

Matches 437; Conservative 25; Mismatches 58; Indels 114; Gaps 10;

OV 1 MNRGVPFRHILLVIOLALLDAATOGNKVVLGKKGDTVELTCTASOKKSIOFHWKNSNOIK 60

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                                                                                           ELLGGPSVFLFPPXPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                         EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                          EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                            -- VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
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PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                         PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
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                                                                                                                                                                                                                                      -- PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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RESULT 20
AAE37574
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
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                                                                                                                                                                                                                                                                                                                               Local Similarity
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DB; AAD29113.
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                              450 AA;
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                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLDETC 632
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                                                                                                                                                                                                                  NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                                                                                              ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                      ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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AAR46679 standard; protein; 530 B

CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; human immunodeficiency virus; radionuclide; toxin; therapy; trainaging; detection; targetting; immunoglobulin; IgG. CD4-IgG2 chimeric heavy chain. treatment;

entry)

(PROG-) PROGENICS PHARM INC 92US-00927931 93WO-US007422 424. .530 /label= CH 205. .302 /label= CH1 Region. /label= CD4 Region. Location/Qualifiers /label= /label= Hinge Region . 423 CH3 Region CH2 Region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image stage HIV infection.
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                                                                                                                                                                                                                                                                                   ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                             DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                    EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNXALPAPIEKTISKAKGQPREPQVYTLP 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL 297
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                                                                                                                                                                        EEQFNSTFRVVSVLTVVHQDWLNGKQYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                                                                                                                                                                                                                                              -- VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                         PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAF -- AST -- -- KGPSV ---
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Pred. No. 9.8e-106;
8; Mismatches 58;
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529
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                                                                                                              The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (Ig) comprising a hinge region and a constant domain of an amammalian Ig heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention are useful for preparing a composition for treating or preventing human immunodeficiency virus (HV)-1 infection. The invention is useful in gene therapy and also in the preparation of vaccines. The present sequence is a fusion protein variant (G218P/L219Y/220deLA/G221A) which comprises a human IgA alpha tailpiece (alphatp), a human IgG2 constant region comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain. This variant protein is also referred to as mutant F
                                                                                                                                                                                                                                                                                                                        New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
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Misc-difference 221
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                                                                                                                                                                                                                                                                                             Example 11; Page 67;
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DB; ACC82877.
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                                 Score 2088; Ub (, pred. No. 7.7e-105;
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RESULT 23
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23-JAN-1989;
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04-FEB-1994;
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       (GEHO)
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       GEN
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                                                                                                                                                                                                                                                                                                                                                                                                            LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPEL----LGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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       HOSPITAL
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                      88US-00147351.

89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
                                                                         9508-00479353
                                                                                                                                 /note=
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                                                                                                                                                                                                  CD4 Pmu;
                                                                                                                                                                                                                                                                   protein; 481
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       CORP
                                                                                                                                         "CD4 extracellular region"
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RESULT 24
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AAY59171;

AAY59171 standard;

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Best Local Similarity
Matches 416; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of fusion protein CD4Pmu comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgM heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgM DNA at the Pst site upstream of the CH2 region (see AAA50663). Fusion protein CD4Pmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgM fusion proteins such as CD4Pmu provide complement-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 481
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N-PSDB; AAA50662.
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                                                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                     QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                           EQYNSTYRVVSVLTV
                                                                                       VFLFPPKPKDTLMIS-RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR----E
                                                                                                                         LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV---
                                                                                                                                           LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLG--GPS
                                                                                                                                                                                     LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                               TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGNQGSFLTKGFSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                             VSVEVP-
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                                                           -PRDGFFGNPRKSKLICQATGFSPR--QIQVSWLREGKQVGSGVTTDQVQAEAK
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Pred. No. 5.4e-104;
9; Mismatches 36;
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Best Local S
Matches 416
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion gene encoding immunoglobulin-CD4 fusion proteins, use the treatment of HIV or simian immunodeficiency virus infections
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DB; AAZ48204.
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                                                                                                                                                                                                                                                                                                                                                             Similarity
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              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVMV 360
                                                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240
                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATOGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                        481
                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 54-60; 89pp;
                                                                                                                                                                                                                                                                                                                                            60.7%;
llarity 84.0%;
Conservative 1
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Pred. No. 5.4e-104;
9; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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13

al Similarity 83.8 415; Conservative

18;

Indels

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120 60

MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK

ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

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RESULT 25
AAY51081
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Best Local S
Matches 415
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                 This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-173 of cD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Pmu which is constructed from CD4 linked
                                                                                                                                                                                                                                                                                    Seed
                                                 Sequence 481
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                                                                                                                                                                                             Example 1; Col 49-58; 39pp; English.
                                                                                                                                                                                                                        Fusion
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                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-1994;
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                                                                        IgM upstream
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89US-00299596.
92US-00896781.
93US-00057952.
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           60.5%;
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                                                                      protein CD4Pmu which of the CH2 region
                                                                                                                                                                                                                      for the treatment of human immunodeficiency virus.
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Score 2067; DB 3;
Pred. No. 1.1e-103;
8; Mismatches 38;
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                     Length 481;
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The fusion protein genes of the invention pref. comprises cDNA which encode CD4 or a fragment which binds gp120 ligated to an plasmid which encodes an antibody in which the variable region gene has been deleted (see WoS7-02671). The CD4 portion of the protein may comprise the complete CD4 sequence, the 370 AA extr
                                                                                                                                                                                                                                                                     WPI; 1989-214472/30.
N-PSDB; AAN90359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein;
diagnosis; CD4;
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03-AUG-1992
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                                                                                                                                                    Example;
                                                                                                                                                                                              Immunoglobulin-CD4 fusion proteins - used for infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construct which encodes m of the CH2 region (fusi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                               Table 4, Page 41-47; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLFPPKPKDTLM-ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR----E
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                                                                                                                                                                                                                                                                                                                                                                                            HOSPITAL CORP
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin-like molecule; HIV; SIV;
gp120; binding fragment; glycoprotein; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codes CD4 linked to human IgM (fusion protein CD4Pmu).
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Best Local Similarity
Matches 415; Conserv
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25-MAR-2003
06-FEB-1993
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                                                                                              Key
Domain
                                                                                                                                                                  Homo sapiens
Chimeric.
                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESSPGSSSPSVQCRSSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGPTTYKVTSTLTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFLFPPKPKDTLMIS-RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNPEAGMMQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLG--GPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                          increased
                                                                                                                                                                                                                                        soluble CD4; T
increased serum
                                                                                                                                                                                                                                                                                                         chimeric heavy chain homodimer.
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                                                                                                                                                                                                                                                                                                                                                   (revised)
(revised)
(first entry)
  Location/Qualifiers
1. .216
/label = CD4
217. .325
/label = CH2
326. .433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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83.8%;
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                                                                                                                                                                                                                                        cell receptor;
half life; HIV
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Pred. No. 1.4e-103;
9; Mismatches 37;
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                                                                                                                                                                                                                                          CD4 antigen; high recovery; infection; AIDS; ss.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It was produced by expression of the coding mutagenised cDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV of. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas extoxin A (domains) I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4-gamma-2 and CD4-IgG2 chimera (s) and expression vectors treatment, prevention and diagnosis of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1991;
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                                                                                                                                                                                                                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKBEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 3;
                   LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                       LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF 420
                                                                                                                                                     LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
                                                                                                                                                                                                                   QAERASSSKSWITFDLKNKEVSVKRVTQDPXLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                          ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFERKCCV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2059; DB 2;
Pred. No. 2.7e-103;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                   coxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                  Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                             A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
                                                                                                                                                                                                                                                                                                                 Disclosure;
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08-AUG-1994
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DB; AAQS7750.
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immunodeficiency virus; radionuclide; toxin; therapy; treatme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g,
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/label= Hinge Region
217. .325
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                                                                                                                  CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
  07-JUN-1995;
                          07-MAR-2000
                                                    US6034223-A.
                                                                            Homo sapiens
                                                                                                     prognosis; envelope glycoprotein burden;
                                                                                                                                                                     Human CD4-gamma 2 chimeric heavy chain homodimer amino acid
                                                                                                                                                                                               19-JUN-2000
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Pred. No. 2.7e-103;
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CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer CC of two heavy chains and two light chains. The cytotoxic radionuclide is CC linked to either the heavy chains or the light chains, or to all four CC chains, directly or through a bifunctional chelator. Both heavy chains CC chains, encoded by vector CD4-IGC (TS193) and both light chains are chimeric CD4-kappa CC chains encoded by vector CD4-kLC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa CC chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-CC polymorphic cell surface glycoprotein that is expressed on the surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and CC dendritic cells. CD4 associates with major histocompatibility complex (CMHC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immune response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating CC (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used to determine the HIV centure staging and prognosis of infection, and for assessing efficacy of interaction burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV (since the CC are assembled intracellularly and secreted efficients). The heterotetramers are assembled intracellularly and secreted efficient mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
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06-AUG-1993;
03-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents the human CD4-gamma 2 chimeric heavy chain dimer amino acid sequence. The invention relates to an
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93WO-US007422.
95US-00379516.
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Sequence 432 ₽ X

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                                                                                                                                                                                                                             61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                             410;
                                                                                                                                                                                                                                                                 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFERKCCV-----
                                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                             Conservative
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                          The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotestramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kLC-pRcWV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                        comprising kappalight
                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                       Bubject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999;
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                                                                                                                                                                                                                                                                        Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoconjugate;
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Query Match

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                        08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                                                                                                   07-JUN-1995;
                                                                                                                                                                    13-FEB-2001.
                                                                                                                                                                                                                US6187748-B1
                                                                                                                                                                                                                                                                                                                                   Human;
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                                                                                                                                                                                                                                                                                                           Human; Anti-HIV; CD4-IgG2 immunoglobulin gamma 2.
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92WO-US001143.
92US-00960440.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves usin CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
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                     QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                        VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                       LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AA;
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                      LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
                                                                                                                                                                                                                                        LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                                                           QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Pred. No. 2.7e-103;
                                                                                                                                                                                                         -----VAGPSVF
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RESULT 32
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10-FEB-1992;
08-DEC-1992;
                                                                   The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV 1) having two heavy chains encoded by an expression vector designated (-IgG2HC-pRcCMV, and two light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or designated CD4-kLC-pRcCMV. (I) and a composition (II) infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                              Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
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                                               Sequence
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DB; ABS55720.
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92WO-US001143.
92US-00960440.
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-IgG2 chimeric heterotetramer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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           65.6%;
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Score 2059; DB 6;
Pred. No. 2.7e-103;
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RESULT 33
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                                                                                                                         22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Mg.
  WPI; 2000-085792/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human fusion
                                                                                                                                                                                                                               04-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                    GEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNPEAGMWOCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKBGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
SASAPTLF-----PLVSC
                                                                   LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHT----CPE
                                                                                                   LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPECPXPKPTPKAKLSTPSARTPG
                                                                                                                                                                                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                        LLGGPSVFLFPPKPKDTLMISRTPEVTC
                                                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2046.5; DB 3;
Pred. No. 1.3e-102;
4; Mismatches 16;
433
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RESULT 34
AAY59170
CA1340741-C
                  Homo
                                     HIV; extracellular; CD4; gp120; immunoglobulin; secreted protein; SIV infection; medicament.
                                                         CD4-Ig
                                                                       14-MAR-2000
                                                                                   AAY59170;
                                                                                                 AAY59170
                  sapiens
                                                         fusion
                                                                                                standard; protein;
                                                         protein CD4Mmu
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein infections in humans. The present sequence represents the fusion protein CD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESSPGSSSSSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                         TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                              | ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                      LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                     QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                                                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TCPPKPTPKAKLS-TPSARTPAPDLS 442
                             LEPPKPKDTLMISRTPEVTCVVVDVS 446
                                                                LNPEAGMWQCLLSDSGQVLLESNÍKVLÞTWSTÞVHA---DPELPLTAHPKGQTLHSLSSD
                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                                   LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                     QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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2.8e-102;
hes 31;
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RESULT 35 AAR27278 ID AAR27

AAR27278

standard; protein; 532

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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1992;
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28-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-331474/40.
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                                                                                              121
                                                                                                                                                                                                                                                                                                                                      397;
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                                                                                                                                                                                                                                                                                                                                                               Similarity
TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                          LVFGLTANSDTHLLQCQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 5.5e-102;
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g HIV-1, AIDS
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RESULT 36
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                                                                                                                      Query Match
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                                                                                                             Matches
                                                                                                                                                                                   Fusion proteins comprising the extracellular domain of CD4 fused to T-cell receptor zeta, gamma or eta (AAR78676-78, respectively) were expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma and CD4:eta chimeric receptors mediated cytolysis of targets expressing
                                                                                                                                                                                                                                                                                                                                    Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-cell receptor
                                                                                                                                                       Sequence 532
                                                                                                                                                                                                                                            Example 2;
                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                             WPI; 1995-292893/38.
                                                                                                                                                                                                                                                                                                                                                                               14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric receptor; CD4; T-cell receptor eta; HIV; cytolysis; human immunodeficiency virus; adoptive immunotherapy.
                                                                                                                                                                                                                                                                             Target cytolysis of HIV-infected cells -
                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1995
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 121
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                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                   Banapour B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPKLC
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                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                            Page 78-79;
                                                                                                            Conservative
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94US-00284391.
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98.3%;
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Pred. No. 5.5e-102;
1; Mismatches 3;
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AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:eta chimera. The transmembrane region of the chimeric receptor acts to separate the contract transmembrane region of the chimeric receptor acts to separate the contract and extracellular domains of the chimera, and contains a portion of the CD7 (see AAR8940), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1 (see AAR8941). The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR89450 and AAR89451) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, neutrophils, or dendritic cells. The therapeutic cells expressing the
                                                                                                                                                                                                                                                                                                      Membrane-bound chimeric receptor comprising extracellular including CD4 fragment - cells expressing receptor can be treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-129034/13.
N-PSDB; AAT10803.
                                                                                                                                                                                                                                                                                                                                                                                                                         Seed B,
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24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
                                                                                                                                                                                                                                                                       Example 2; Page 80-81; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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RESULT 38
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Matches 397
                                                                                                                                                                                                                   07-MAR-1991;
06-MAR-1992;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; zeta; eta; gamma; membrane-bound chimeric receptor; infe tumour; cancer cell; autoimmune-generated cell; T cell receptor CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
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92US-00847566.
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                                                                                                                                                                Pusion protein; CD4; extracellular domain; zeta; eta; gamm membrane spanning domain; intracellular domain; type I; integral membrane homodimer; TCR; T cell antigen receptor; extracellular domain; mouse; human; receptor; chimera; HPB-ALL tumour cell line; natural killer cell.
                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
28-JUL-1995
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                                                                                                                                                                                                                                                                                                                                              CD4:zeta peptide chimeric protein
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